

6 ANALYZING 2D SCAN DATA

Once a scan has been completed, the computer processes the measurement data and displays it in the Data Analysis window. This chapter discusses how information is presented in the Data Analysis window and how to analyze and manipulate the data.

This chapter describes

- Parts of the Data Analysis window
- Leveling the data
- Using the measurement cursors
- Using Feature Detection
- Using cutoff filters on the data
- Radius measurements on curved surfaces
- Saving and maintaining data

6.1 DATA ANALYSIS WINDOW

When a scan is completed, the Data Analysis window appears:

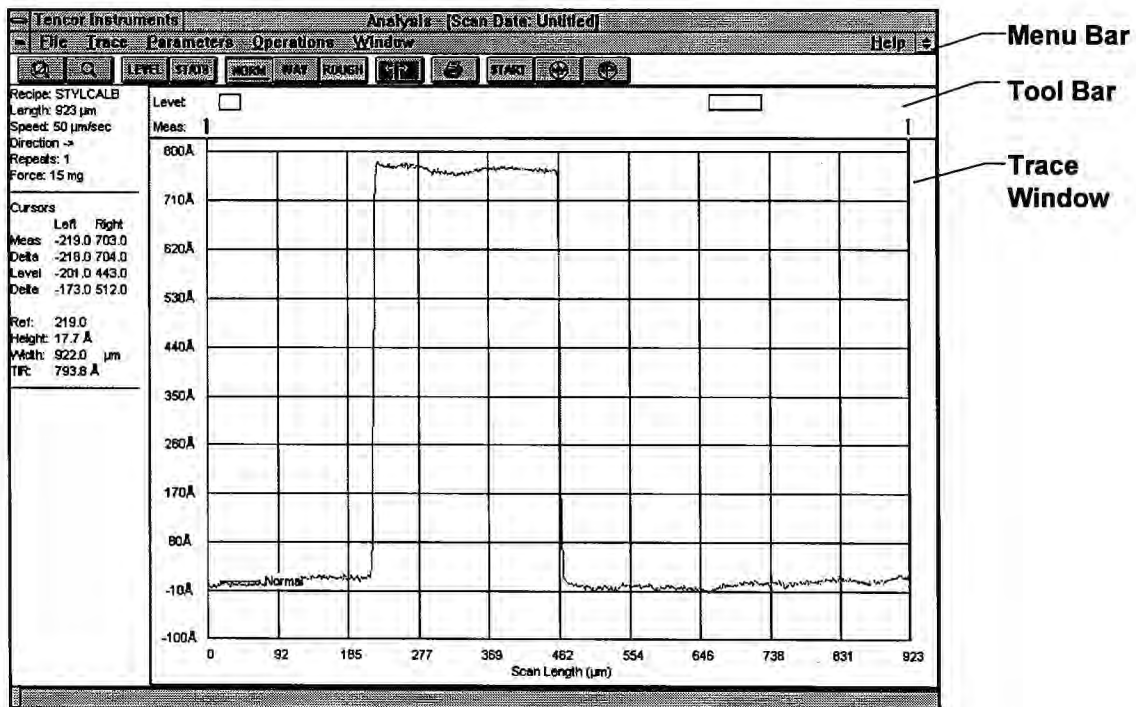


Figure 6-1 2D Data Analysis Window

You can also review previously saved data in the Data Analysis window.

To review previously saved data:

1. From the Database Catalog window, select Scan Data. The Scan Data Catalog is displayed:

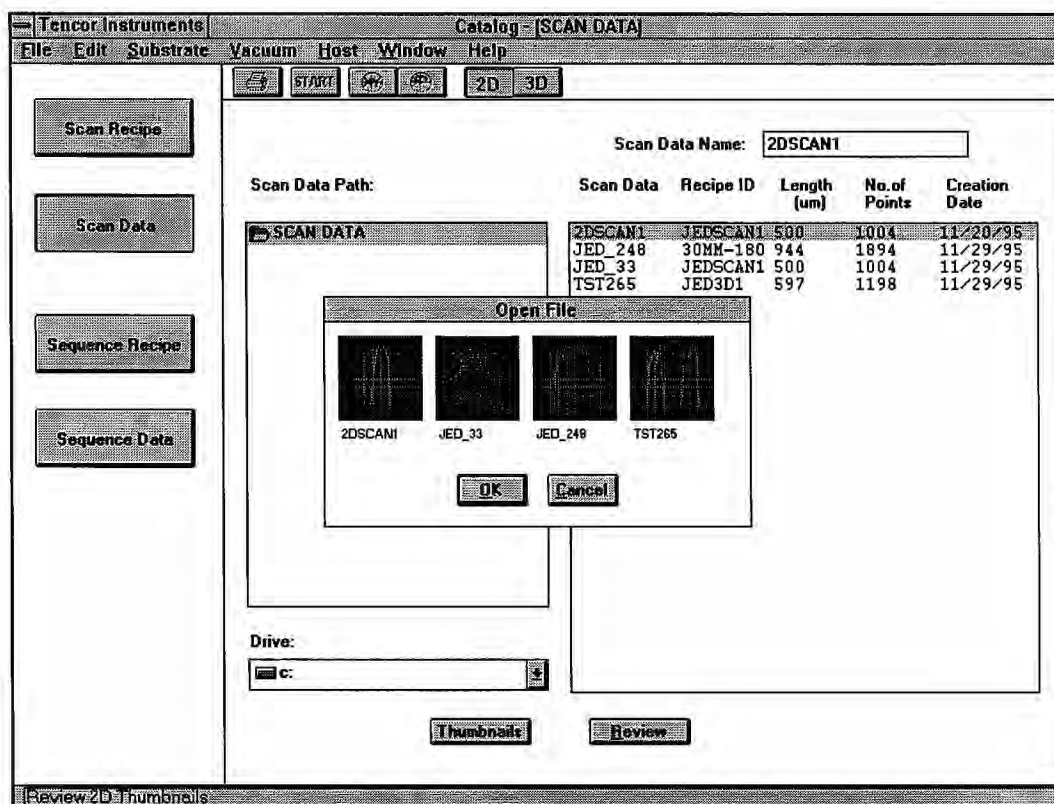


Figure 6-2 Scan Data Catalog Window

2. If necessary, click on the 2D or 3D button (or choose 2D and 3D in the File menu) to display the catalog desired.
3. To select and open a data set, use either of the following methods:
 - Click on the Thumbnails button to display small graphical representations of each data set. Then click first on the thumbnail desired, then on OK to open the file. You can also double-click on the thumbnail to open the file.
 - or
 - Click on the name of the desired data set in the list, and then click on the Review button below the list, or double-click on the name of the desired data set.

The Data Analysis window appears with the selected data set displayed.

6.1.1 DATA ANALYSIS MENU BAR

The Data Analysis menu bar provides the following menus. You can view menus by clicking on the titles in the menu bar, or by pressing ALT + *l*, where *l* is the letter that appears with an underscore in the desired title in the menu bar. You can choose menu items by clicking on a menu entry or by typing the letter that appears with an underscore in the desired menu item.

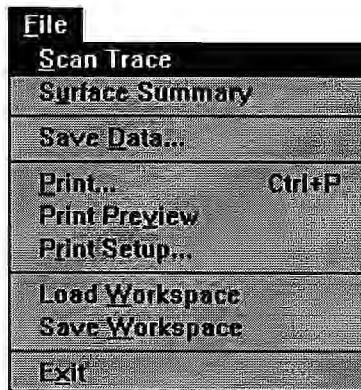


Figure 6-3 File Menu



Figure 6-4 Trace Menu

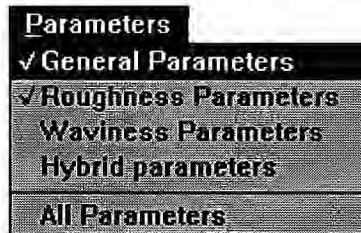


Figure 6-5 Parameters Menu

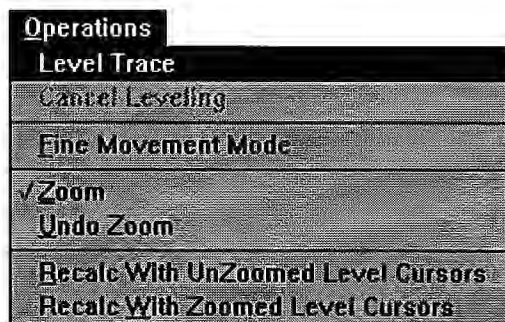


Figure 6-6 Operations Menu

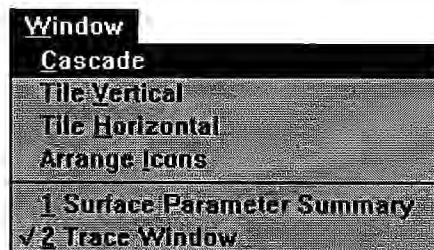











Figure 6-7 Window Menu

6.1.2 DATA ANALYSIS TOOL BAR

The Data Analysis tool bar contains a row of icons that resemble buttons. Clicking on these buttons provides an alternative way to access commonly used functions. Each icon suggests the function of the button. Buttons that appear dimmed are unavailable.

The Data Analysis tool bar contains the following buttons.

Button	Action
	Returns scan plot to original scale from zoomed in view.
	Activates cursors for selecting a scan segment for magnification.
	Toggles between the Measurement and Leveling cursors.
	Switches focus to the Surface Parameter Summary window. If the Surface Parameter Summary window is currently minimized, it appears maximized upon clicking this button.
	Toggles display of normal trace.
	Toggles display of waviness trace.
	Toggles display of roughness trace.
	Activates Fine Movement Mode.
	Displays the Print dialog box.

6.2 DATA LEVELING AND MEASUREMENT

This section discusses leveling and measurement of the scan data. Data leveling completes the adjustment begun by the mechanical leveling of the stage performed prior to the scan (Section 5.7, "Leveling the Stage").

To accurately measure anything, you need to have a sensible frame of reference. For 2-D scan data, this amounts to indicating two points along the scan that are at equal heights. These two points define a reference axis for plotting the data and calculating surface parameters.

In the Tencor P-20h Data Analysis window, the two points are indicated by using two pairs of vertical lines called the leveling cursors. The initial position of the leveling cursors is set in the recipe, but you are free to reset their positions at any time after the scan is taken.

Each 2D cursor, measurement or leveling, consists of a pair of vertical lines that can be expanded to define a region. The average value of the height within the region is then used

for measurement and leveling. For best results on rough or noisy scans, you should expand the cursors to cover a wider region.

Often you can determine acceptable leveling cursor positions in advance by viewing a sample in the XY View window prior to finalizing the recipe and scanning. However, it is not always obvious, or you might accidentally set them at inappropriate locations. In an extreme case, the left leveling cursor might be at the bottom of a large step, and the right leveling cursor on the top. Using these two areas to define a reference axis, the plotted data looks something like the following figure.

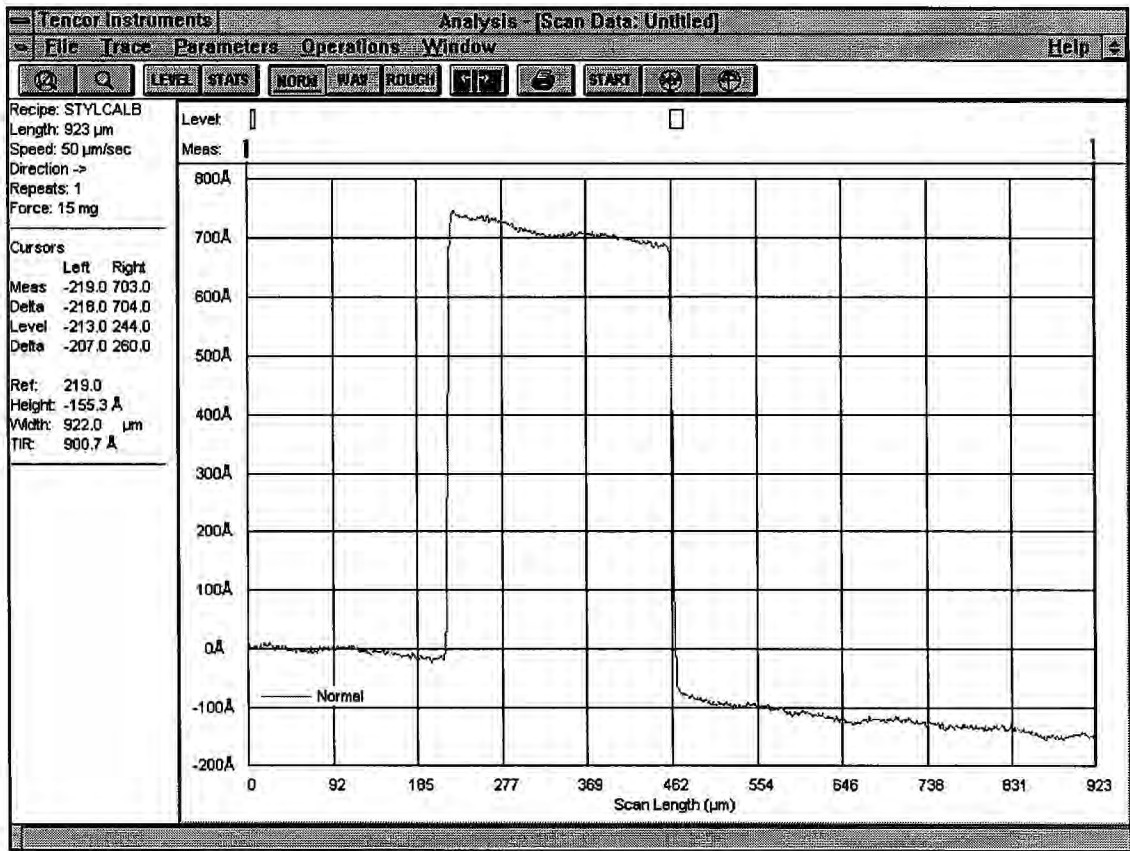


Figure 6-8 Data Before Leveling

Fortunately, you have complete control of the leveling cursors, so you can readjust them until they indicate two points that are at the same height. Then you have the computer replot the data with these new positions, and the result is something like the following figure.

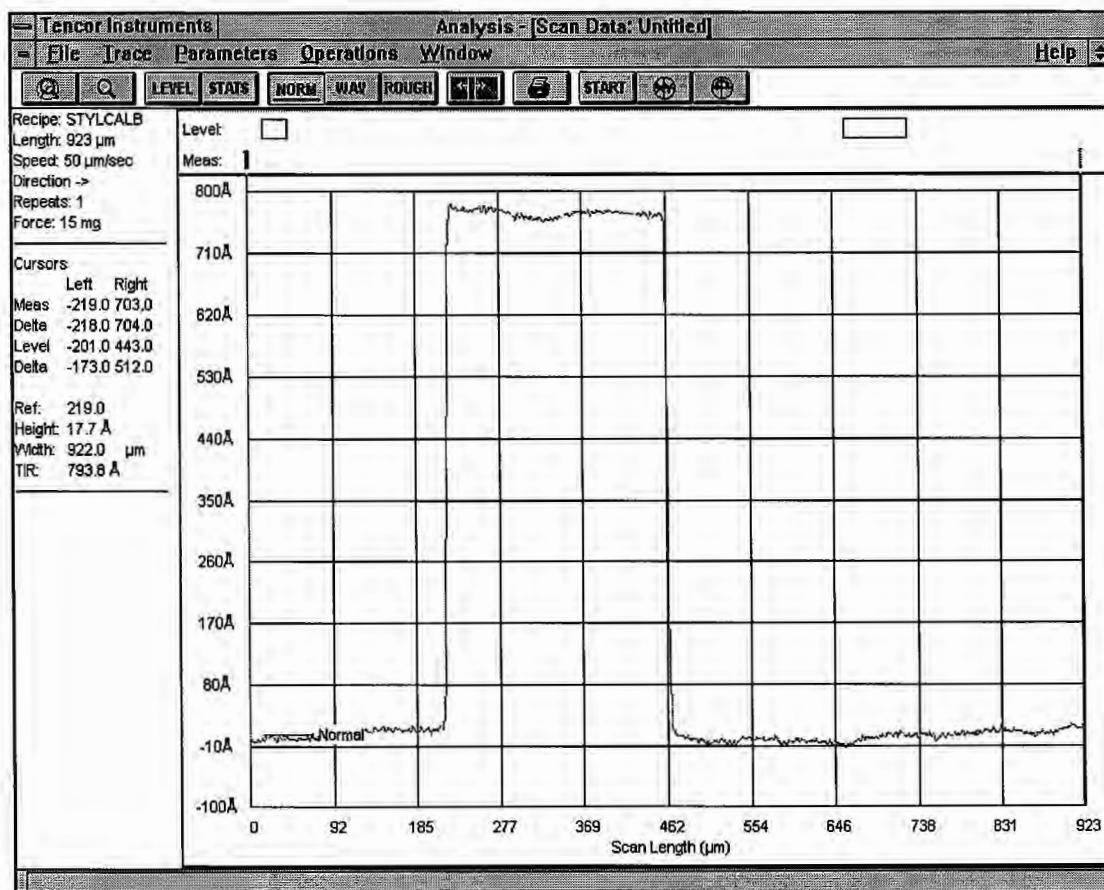


Figure 6-9 Data After Leveling

This Data Analysis window can now provide you with some meaningful measurements. Again, you need a way to indicate to the computer what you want to measure. For example, if you want to know the difference in height between two points, you need to be able to indicate those two points to the computer.

This is accomplished using another set of vertical lines, the *measurement cursors*. The Data Analysis window appears with the measuring cursors set at the locations specified in the scan recipe.

Like the leveling cursors, the measurement cursors can be freely moved to any position. The displayed parameter values are recalculated whenever the measurement cursors are moved to new locations.

To set leveling or measurement cursors:

The measurement cursors normally are active unless you have selected the leveling cursors to level the scan. Reactivate the measurement cursors by clicking on LEVEL in the tool bar.

1. To set the leveling cursors, select Level Trace from the Operations menu, or click on LEVEL in the tool bar. This activates the leveling cursors. They are at the locations currently specified in the recipe, with the left cursor selected.

To reactivate the measurement cursors, use Level Trace or LEVEL as above.

2. Press [<] or [>] or use the trackball, with cursor on the bar or inside the pair of lines, to move the left cursor to the desired position.
3. To adjust the width of the cursor:
 - Place the cursor near and outside of the line to be moved.
 - Click and drag to the new position.

4. Repeat steps 1 through 3 with the right cursor. You can also move the cursors in tandem:
 - Press the spacebar until both cursors are selected. Use the arrow keys to position them.

If you need finer cursor control, select Fine Movement Mode from the Operations menu or click on its icon in the tool bar (a miniature scan trace). Press [<] or [>] to position the cursor pair.

5. **To level the scan:**
 - Once the cursors are positioned as desired, select Level Trace from the Operations menu, or click on the Level button in the tool bar. The data is leveled and replotted. The leveling cursors become inactive and the measurement cursors become active.

To measure:

- Set the measurement cursors on the desired features. The parameter values are displayed in the Trace Information area to the left of the scan.

If desired, you can replace the cursor positions stored in the recipe with the new positions of the cursors.

To save the current cursor positions in the Scan recipe and update the data in the Surface Parameter Summary window:

Choose Recalc with Unzoomed Level Cursors from the Operations menu.

To zoom in on selected features:

1. Click on Zoom In on the tool bar or choose Zoom In from the Operations menu. Two vertical lines appear on the scan.

2. Ignore the two lines and position the cursor to one side of the feature you want to enlarge.

Click and drag the cursor across the feature. The two vertical lines reappear, one at the starting point and one that follows the cursor as you drag it.

3. Click again to drop the second cursor at your ending point and to zoom the scan.

You can also position the vertical lines with the arrow keys. Pressing the spacebar zooms the scan.

Note: For finer positioning, select Fine Movement Mode from the Operations menu or click its icon on the toolbar (a miniature scan trace). Press [$<$] or [$>$] to position the vertical lines.

4. Return to the original scan view by clicking on Undo Zoom or select Undo Zoom from the Operations menu.
5. To update the data in the Surface Parameter Summary window and to enter new leveling cursor positions in the recipe, select Recalc with Zoomed Level Cursors from the Operations menu.

XY View Parameter Values

Meas	X-axis value of the left vertical line of the selected measurement cursor.
Delta	X-axis value of the right vertical line of the selected measurement cursor.
Level	X-axis value of the left vertical line of the selected leveling cursor.
Delta	X-axis value of the right vertical line of the selected leveling cursor.
Ref	Scan position reference point designated in the recipe.
Height	Difference between the average height of the scan region marked by the right measurement cursor and the average height of the scan region marked by the left measurement cursor.
Width	Difference between the average X value of the scan region marked by the right measurement cursor and the average height of the scan region marked by the left measurement cursor.
TIR	Total Indicated Runout. The difference between the highest and the lowest points on the scan.

6.3 USING FEATURE DETECTION

Consider a situation where you wish to compare the step heights from ten different instances of an artifact on a sample. It is difficult without taking extra care to start each of the ten scans at precisely the same location relative to the artifacts. Typically, the measurement cursor settings from the first scan will not precisely compare to the same locations relative to the feature on the subsequent scans. Therefore, you need to manually adjust the measurement cursors for each scan. This can be tedious and introduces some imprecision into the comparison, since it is difficult to locate the cursors manually in exactly the same way for all the scans.

Feature Detection makes it possible to automatically and reliably set the position of the measurement cursors relative to the rising or falling edge of a steplike feature, or the apex of an arclike feature. For each instance, then, you need not worry that you are starting the scan at precisely the same distance in front of each of the artifacts. This eliminates the need to manually adjust the cursors for each scan, facilitating comparison between two or more instances of an artifact.

Both the location of the edge (or the apex of an arc) and the step width can be calculated and displayed in the Data Analysis window.

For steplike features, Feature Detection distinguishes between rising or falling edges. Since steps are rarely perfectly vertical, Feature Detection also distinguishes between two types of edges. The following convention is used: the location at the *top* of the slope is called the edge, and the location at the *bottom* of the slope is called the base. The following figure shows this convention for a plateau and a valley.

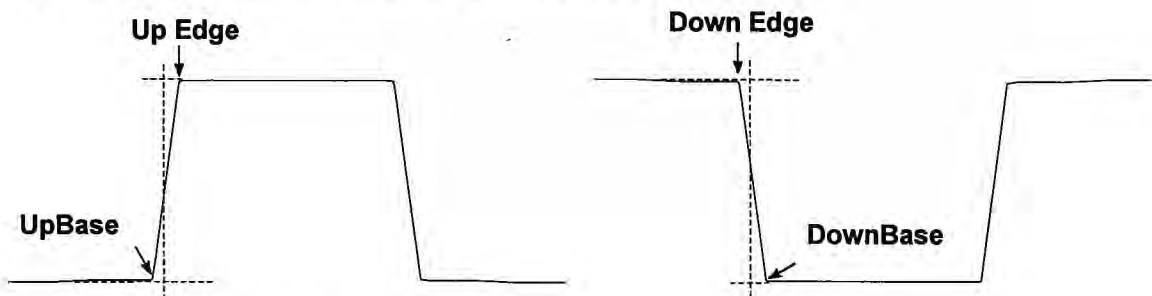


Figure 6-10 Edges of a Step

Feature Detection also distinguishes between convex (hill-like) and concave (valley-like) arcs (Fig 6-11).

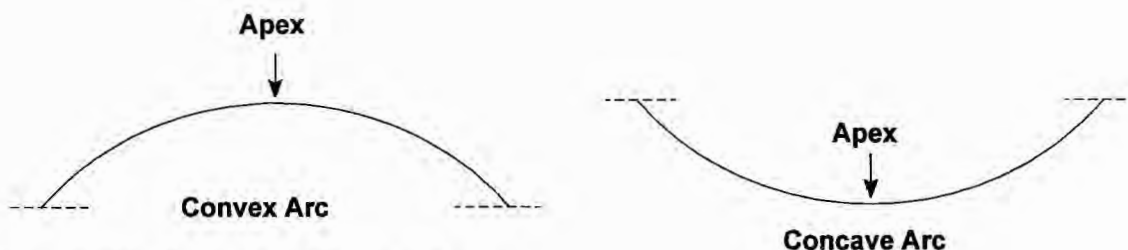


Figure 6-11 Convex and Concave Arcs

Feature Detection parameters are configured in the Recipe Editor window:


Feature Detection	
Feature:	
Feature Number:	<input type="text" value="1"/>
Slope Threshold :	<input type="text" value="10."/>
Plateau Threshold :	<input type="text" value="10."/>
Min. Plateau Width :	<input type="text" value="10."/>

Figure 6-12 Feature Detection Dialog Box

You must set several values to specify the type of the step edge or apex feature that you are measuring. A description of these values follows.

Feature

The Feature field identifies the type of feature to be detected, or turns Feature Detection off. The selection box has seven possible choices:

- None (no Feature Detection)
- UpEdge (rising edge)
- DownEdge (falling edge)
- UpBase (rising base)
- DownBase (falling base)
- Convex (hill-like arc)
- Concave (valley-like arc)

If None is selected, the remaining fields in the dialog box are unavailable and appear dimmed.

Click anywhere in the selection box and click on the desired item in the list or double-click in the selection box and type the first letter or letter of the desired item in the list.

Feature Number

If there are multiple edges detected in a scan, Feature Number provides a way to select a particular edge for detection. Detected edges are numbered sequentially from 1 to n.

Slope Threshold

This factor sets the value at which an upward slope in the trace is considered to be preceding the step height edge or apex; that is, when an upward slope appears that rises significantly above the general roughness of the surface.

Valid values range between 0–50.000. When the artifact is much larger in comparison to the surrounding roughness of the surface, set the value higher. If the artifact is only a little larger than the surrounding roughness, set this value lower. Note that in this case, you might also need to set the Minimum Plateau Width (description follows) to avoid any ambiguity.

The concept of the Slope Threshold is very similar to a signal-to-noise ratio. The best values for a given sample will depend on the relative scales of the artifact that you are examining and the surrounding surface roughness, as well as parameters such as scan speed, sampling rate, and so on. You might need to experiment to find appropriate values for Slope Threshold. The default values of 5.000 (for a step) and 1.000 (for an apex) are sufficient for most scans above 200Å.

Click in the Slope Threshold field and type the desired value.

Plateau/Apex Threshold

This factor affects the precise horizontal location calculated for the edge or arc. Since the edge of a step is rarely a perfectly defined location, this factor allows you to adjust the value to the left or right, depending on whether you consider the edge to be the bottom of the step, the top of the step, or somewhere in between.

For an edge, set this value to about the same value as the Slope Threshold. Valid values range between 0–50.000. Setting this threshold slightly greater than the Slope Threshold will move the precise location of the edge slightly to the left for an UpEdge or to the right for a DownEdge. Setting this threshold slightly smaller than the Slope Threshold will move the precise location of the edge slightly to the right for an UpEdge or to the left for a DownEdge. For UpBase and DownBase, the adjustment is the reverse. For a Concave or Convex arc, set this value to a very small number, between 0–1.000. You might need to experiment to find appropriate values for Plateau/Apex Threshold depending upon the relative scales of the artifact that you are examining and the surrounding surface roughness. The default values of 5.000 (for a step) and 0.000 (for an arc) are sufficient for most scans above 200Å.

NOTE: The Slope Threshold determines whether or not an edge is detected; the Plateau/Apex Threshold determines only the precise reported location of a detected edge.

Click in the Plateau/Apex Threshold field and type the desired value.

Minimum Plateau Width

This value specifies the minimum horizontal length between a rising and falling edge, used in the feature detection calculation to determine the correct edge. This is useful in cases when the roughness of a surface might be large enough that it becomes difficult to adjust the Slope Threshold to find the correct feature without ambiguity. In such cases, narrow roughness peaks can extend above the height determined by the Slope threshold without causing the algorithm to identify them as the edge.

For steplike features, the Minimum Plateau Width specifies a plateau as follows:

- For ascending features (UpEdge, UpBase), the plateau is the one following the detected edge.
- For descending features (DownEdge, DownBase), the plateau is the one preceding the detected edge.

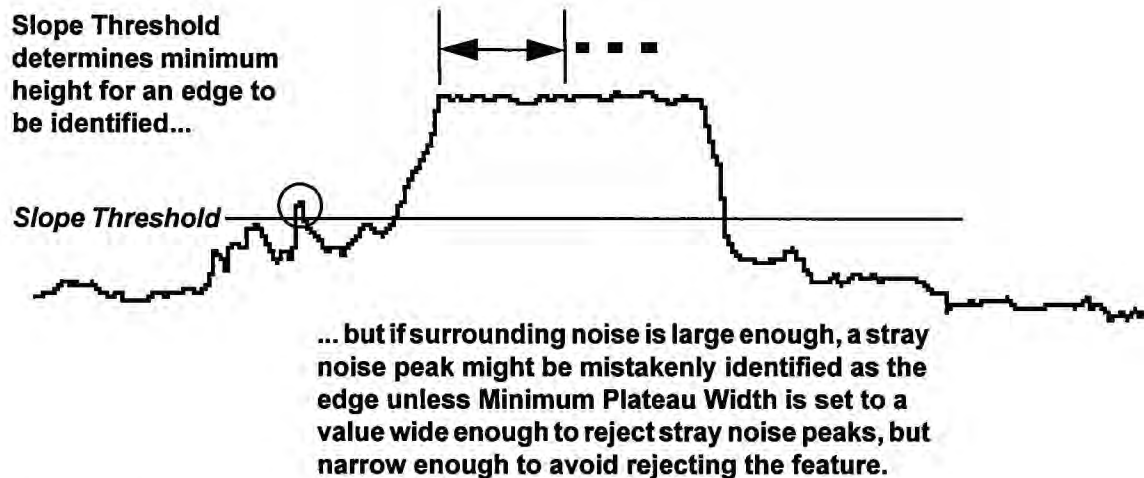


Figure 6-13 Feature Detection and Minimum Plateau Width

The Minimum Plateau Width can be used to reject such peaks that may otherwise cause failure to detect the correct edge. For UpEdge, DownEdge, UpBase, or DownBase features, set this value to be greater than the width of stray peaks, but always slightly less than the width of the step to be detected. Set this value to slightly less than the step width. Setting it too high will result in no edge being found. Valid values are in the range 0.005–1000.00 μm (0.0002–39.3701 mil).

NOTE: Minimum Plateau Width is not intended for use with Concave or Convex features. In cases of rough sample surfaces, though, it might be useful. For a Convex arc, the Minimum Plateau Width specifies a minimum width for the feature, and so can be used to reject narrow roughness peaks in the vicinity of the arc. For a Concave arc, the Minimum Plateau Width is used to specify a minimum size for a level section following a detected arc.

Click in the Minimum Plateau Width field and type the desired value.

When Feature Detection is enabled, the following General Parameters are interpreted as follows.

Edge (Distance to Edge)

Depending on the setting of the Slope Threshold and the Plateau/Apex Threshold, this distance is either

- The distance between the beginning of the scan and the first rising or falling edge or base of a step; or
- The distance between the beginning of the scan and the apex of the first convex or concave arc.

StpWt (Width of Step)

The width of a step plateau; that is, the distance between the leading and trailing edges of the plateau. The StpWt value does not apply in the case of an arc.

NOTE: It is important that you can use the Feature Detection calculation reliably if you have set the thresholds appropriately for the particular type of feature you are scanning. Also note that the profile scan length must be long enough that the artifact is completely included, and that there is enough scan data on either side for the leveling cursors to be set reliably.

The following figures (Figs. 6-14 through 6-16) demonstrate the usefulness of Feature Detection. The three scans were taken across the same section of the artifact, but the scans began and ended at different points along the profile.

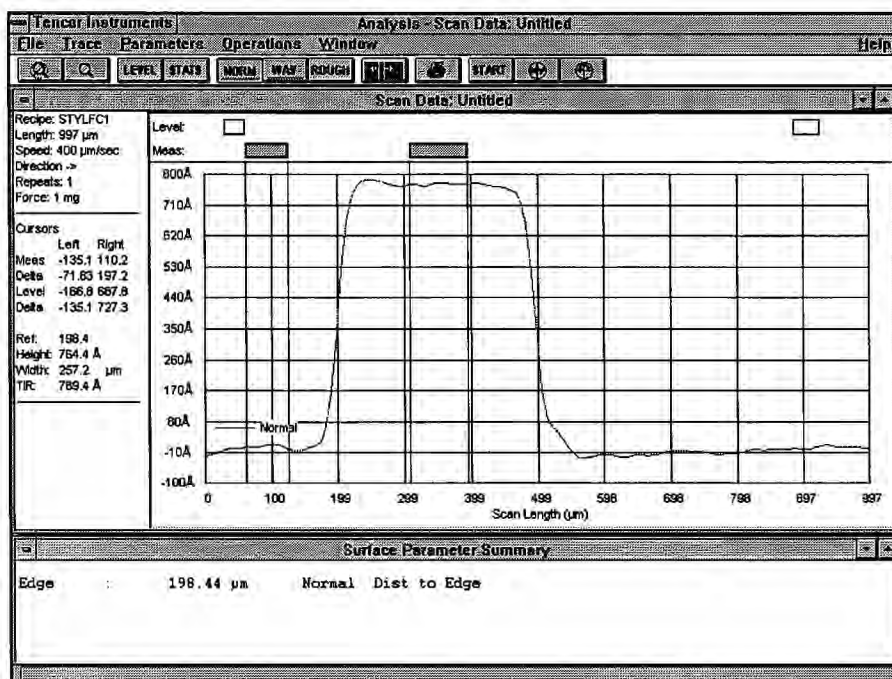


Figure 6-14 Scan 1 with Feature Detection Enabled

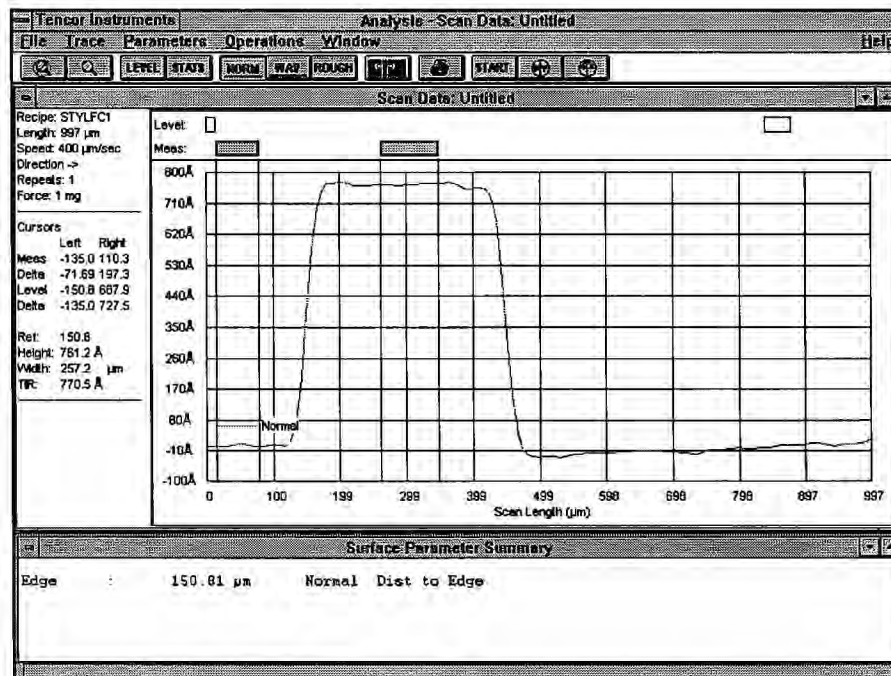


Figure 6-15 Scan 2 with Feature Detection Enabled

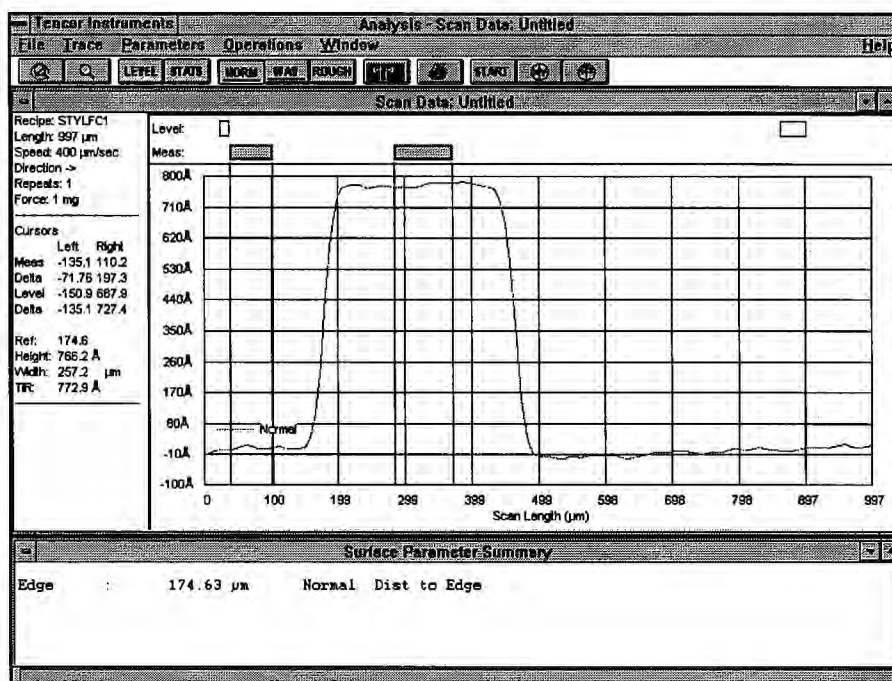


Figure 6-16 Scan 3 with Feature Detection Enabled

6.4 USING CUTOFF FILTERS

The Tencor P-20h scan data does not come directly from the sensor, but instead is filtered through three stages:

- an analog hardware filter
- a digital decimation filter
- digital software filtering

The sensor output is filtered by the analog hardware filter so that it can be digitized with minimal distortion. The filter also reduces noise by attenuating higher frequencies. It has a fixed cutoff frequency of 18 Hz.

The signal then passes through an analog-to-digital (A/D) converter. The A/D converter has a nominal sampling frequency of 200 Hz (100 Hz at the 1 $\mu\text{m/s}$ and 2 $\mu\text{m/s}$ scan speeds).

Next, the signal passes into the digital decimation filter. This step is necessary to reduce the signal sampling rate from the original 200 Hz (or 100 Hz) down to the sampling rate selected in the recipe by the user. If you select the maximum sampling rate in the recipe, no decimation is done.

Along with reducing the sampling rate, the decimation filter also affects the cutoff frequency of the scan data. At 100 Hz, the cutoff frequency is not significantly reduced, but at 50 Hz, the cutoff frequency is reduced to 14 Hz.

The cutoff wavelength depends on the scan speed as described by the following equation:

$$\text{Cutoff Wavelength} = \frac{\text{Scan Speed}}{\text{Cutoff frequency of combined filters}}$$

For example, with a scan speed of 100 $\mu\text{m/s}$, and a sampling rate of 200 Hz or 100 Hz, the cutoff wavelength is 5.6 μm . With this same scan speed, however, at a sampling rate of 50 Hz, the cutoff wavelength is 7.1 μm .

The action of a cutoff filter can be illustrated by plotting the percentage of signal transmission as a function of wavelength (usually plotted as the logarithm of wavelength). Note that there is always some slope in the transmission curve of a cutoff filter; that is, the transmission percentage is not exactly zero for all values on one side of the cutoff value and exactly 100 for all values on the other side of the cutoff value. The cutoff wavelength of a filter is defined by that wavelength at which 50% of the signal is passed.

The following figure shows the transmission curve of the combined analog and decimation filters. For every factor of 10 in scan speed, the curve moves to the right by a factor of 10 in wavelength.

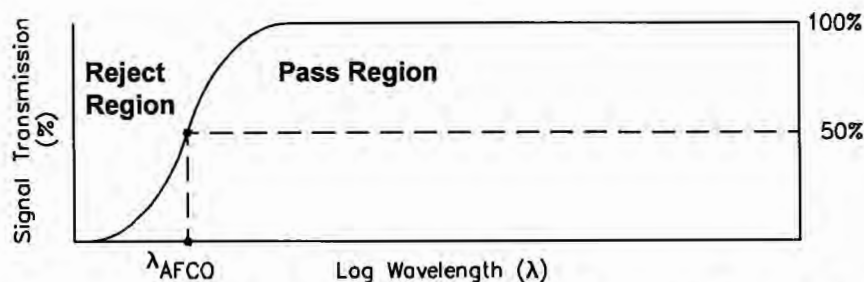


Figure 6-17 Effect of the Analog Filter and Decimation Filter on Signal Transmission

Two adjustable software cutoff filters—short wave and long wave—allow you to control the range of wavelengths collected in your scan data. You might wish to filter data to

- reduce the effect of small surface irregularities or environmental noise
- remove large-scale waviness and form error so that roughness can be evaluated unambiguously
- isolate specific frequency bands, allowing determination of intermediate components of roughness or waviness

The *short wave cutoff* (or long wave pass) filter, as the name implies, cuts off the short wavelengths in the data (those below the filter's *cutoff value*), passing the longer wavelengths.

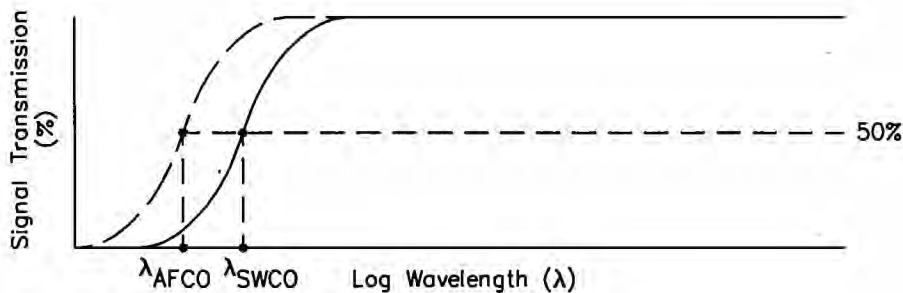


Figure 6-18 Effect of the Short Wave Cutoff Filter

Conversely, the *long wave cutoff* (or short wave pass) filter cuts off the higher wavelengths in the data (those above the filter's cutoff value), passing the shorter wavelengths.

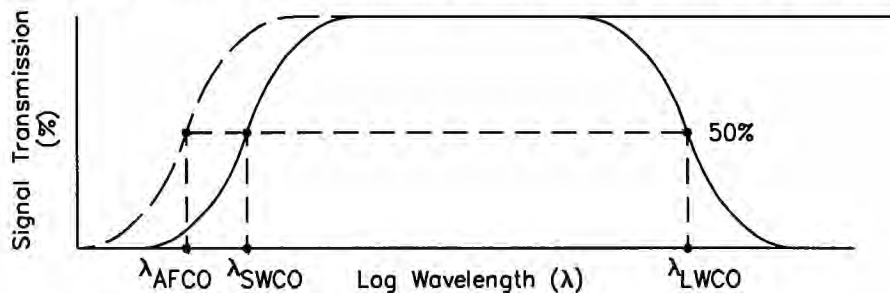


Figure 6-19 Effect of the Long Wave Cutoff Filter

The P-20h gives you a choice of two kinds of long wave filters: Gaussian, for Windows-based systems; and RC, for data files comparable to those obtained with DOS-based systems such as the Tencor P-2 Long Scan Profiler.

You can use the long- and short wave filters separately, or together to form a *band pass* filter that cuts off all short wavelengths below the short wave cutoff value *and* all long wavelengths above the long wave cutoff value. Note that the software will not allow setting a short wave cutoff that is larger than the long wave cutoff, which, of course, would result in a zero-width band of wavelengths, attenuating all of the data.

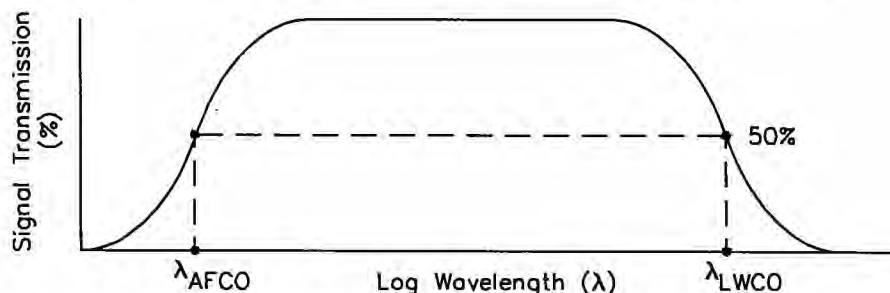


Figure 6-20 Defining a Pass Band with the Short Wave and Long Wave Cutoff Filters

To set the short wave filter cutoff values:

1. From the recipe window, click on Filters/Cursors to open a dialog box.
2. Tab to the Noise entry field to enter a wavelength (in μm), or click on the drop-down arrow to choose a value from the range of cutoff filters provided. You can also turn off the filter. Selectable values are listed in Table 6-1.

Table 6-1 Short Wave Cutoffs

μm	mil	μm	mil	mm	mil
Default ¹	—	14	.56	1.4	56
0.25	.01	25	1.0	2.5	100
0.45	.02	45	1.8	4.5	180
0.80	.03	80	3.0	8.0	300
1.4	.06	140	5.6	14	560
2.5	.10	250	10.0	25	1000
4.5	.18	450	18.0	—	—
8.0	.30	800	30.0	—	—

¹ Refer to Table 6-2 for default short wave cutoff values.

Up to 22 possible settings (including the default) are available depending on the scan speed. You are prevented from mistakenly entering a short wave cutoff that is longer than the currently selected long wave cutoff, or shorter than the value of the analog cutoff. For scan speeds greater than 5 $\mu\text{m/s}$, the shortest short wave cutoff selection turns off the short wave cutoff filter.

If subsequent changes to the scan speed or scan length cause the short wave cutoff setting to become invalid, the cutoff is automatically changed to the nearest available valid value (possibly the default).

The default cutoff depends on the scan speed and sampling rate. The full range of default short wave cutoffs is listed in Table 6-2.

Table 6-2 Default Short Wave Cutoffs

Scan Speed ($\mu\text{m/s}$)	Sampling Rate (Hz)	Short Wave Cutoff Frequency (Hz)		Short Wave Cutoff Wavelength (μm)	
		RC	Gaussian	RC	Gaussian
1	50	4	6	0.25	0.17
	100	7.5	12	0.13	0.08
	200	15	24	0.067	0.042
	500	37.5	60	0.027	0.017
2	50	4	6	0.5	0.33
	100	7.5	12	0.27	0.17
	200	15	24	0.13	0.083
	500	37.5	60	0.053	0.033
	1000	75	120	0.027	0.017
5	50	4	6	1.3	0.83
	100	7.5	12	0.67	0.42
	200	15	24	0.33	0.21
	500	37.5	60	0.13	0.083
	1000	75	120	0.067	0.042
10	50	4	6	2.5	1.7
	100	7.5	12	1.3	0.83
	200	15	24	0.67	0.42
	500	37.5	60	0.27	0.17
	1000	75	120	0.13	0.08
20	50	4	6	5.0	3.3
	100	7.5	12	2.7	1.7
	200	15	24	1.3	0.83
	500	37.5	60	0.53	0.33
	1000	75	120	0.27	0.17
50	50	4	6	13	8.3
	100	7.5	12	6.7	4.2
	200	15	24	3.3	2.1
	500	37.5	60	1.3	0.83
	1000	75	120	0.67	0.42
100	50	4	6	25	17
	100	7.5	12	13	8.3
	200	15	24	6.7	4.2
	500	37.5	60	2.7	1.7
	1000	75	120	1.3	0.83

Table 6-2 Default Short Wave Cutoffs

Scan Speed ($\mu\text{m/s}$)	Sampling Rate (Hz)	Short Wave Cutoff Frequency (Hz)		Short Wave Cutoff Wavelength (μm)	
		RC	Gaussian	RC	Gaussian
200	50	4	6	50	33
	100	7.5	12	27	17
	200	15	24	13	8.3
	500	37.5	60	5.3	3.3
	1000	75	120	2.7	1.7
400	50	4	6	100	67
	100	7.5	12	53	33
	200	15	24	27	17
	500	37.5	60	11	6.7
	1000	75	120	5.3	3.3
1000	50	4	6	250	170
	100	7.5	12	130	83
	200	15	24	67	42
	500	37.5	60	27	17
	1000	75	120	13	8.3
2000	50	4	6	500	330
	100	7.5	12	270	170
	200	15	24	130	83
	500	37.5	60	53	33
	1000	75	120	27	17
5000	50	4	6	1300	830
	100	7.5	12	670	420
	200	15	24	330	210
	500	37.5	60	130	83
	1000	75	120	67	42
10000	50	4	6	2500	1700
	100	7.5	12	1300	830
	200	15	24	670	420
	500	37.5	60	270	170
	1000	75	120	130	83
25000	50	4	6	6300	4200
	100	7.5	12	3300	2100
	200	15	24	1700	1000
	500	37.5	60	670	420
	1000	75	120	330	210

To set the long wave filter cutoff values:

1. From the recipe window, click on Filters/Cursors to open a dialog box.
2. Tab to the Waviness entry field to enter a wavelength (in μm), or click on the drop-down arrow to choose a value from the range of cutoff filters provided. You can also turn off the filter. Selectable values are listed in Table 6-3.

Table 6-3 Long Wave Cutoffs

μm	mil	μm	mil	mm	mil	mm	mil
4.5	0.18	80 ¹	3.0 ¹	1.4	56	25.0	1,000
8.0	0.30	140	5.6	2.5	100 ¹	45.0	1,800
14	0.56	250 ¹	10.0 ¹	4.5	180	-	-
25	1.0	450	18.0	8.0	300	-	-
45	1.8	800 ¹	30.0 ¹	14.0	560	-	-

¹Cutoffs specified in ANSI B46.1-1985

Up to 17 filter choices are available depending on the scan speed. You are prevented from mistakenly entering a long wave cutoff that is shorter than the currently selected short wave cutoff or the value of the analog cutoff.

If subsequent changes to the scan speed or scan length cause the long wave cutoff setting to become invalid, the cutoff is automatically changed to the nearest available valid value.

The following figures show the effect of different cutoff filter settings on the same set of scan data.

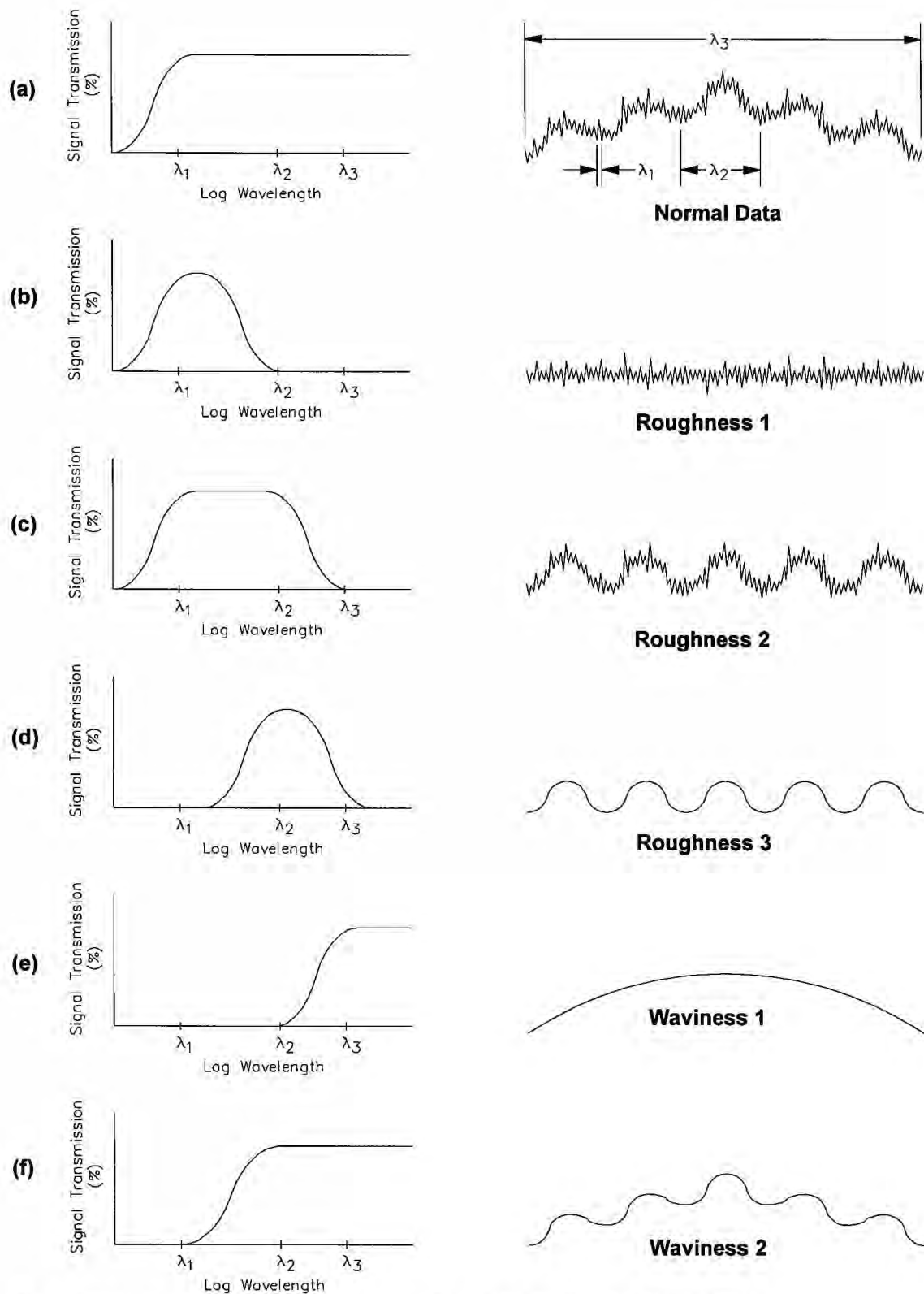


Figure 6-21 Signal Transmission Curves and Their Effects on Scan Data

In Figure 6-21(a), only the analog filter acts on the data. Three wavelengths, labeled λ_1 , λ_2 , and λ_3 , are identified.

In Figure 6-21(b), the long wave cutoff filter is applied with a cutoff value just higher than λ_1 . The resulting data trace shows only features of the scale of λ_1 ; higher wavelengths, including λ_2 and λ_3 , are suppressed.

In Figure 6-21(c), a different long wave cutoff value is applied, this time just higher than λ_2 . The resulting data trace shows features of the scale of λ_1 to λ_2 ; higher wavelengths, including λ_3 , are suppressed.

In Figure 6-21(d), a short wave cutoff filter with a cutoff just higher than λ_1 is applied in addition to the long wave cutoff from Figure 6-21(c). The resulting data trace shows only features of the scale of λ_2 ; higher wavelengths, including λ_3 , and lower wavelengths, including λ_1 , are suppressed.

In Figure 6-21(e), the short wave cutoff filter is applied with a cutoff value just lower than λ_3 . The resulting data trace shows only features of the scale of λ_3 ; lower wavelengths, including λ_1 and λ_2 , are suppressed.

Finally, in Figure 6-21(f), the short wave cutoff filter is applied with a cutoff value just lower than λ_2 . The resulting data trace shows features of the scale of λ_2 and λ_3 ; lower wavelengths, including λ_1 , are suppressed.

6.5 RADIUS MEASUREMENT ON CURVED SURFACES

The average radius of a circular segment defined by the measurement cursors is calculated from a data set using the least squares fit method. This method is capable of high precision. It is useful over a range from 0.5 μm (20 $\mu\text{in.}$) to 200 mm (7.9 in.), provided that the sample will fit into the instrument.

You should keep in mind that the radius of the measurement stylus is added to the sample radius in the measurement. While the radius of a 2- μm stylus added to a 20-mm radius sample might be considered negligible (0.01%), that of a 5- μm stylus added to a 1-mm radius is a 0.5% error, which is probably not acceptable.

This consideration disappears if the instrument is calibrated with a high precision cylindrical standard whose radius is within a factor of 5 of the sample to be measured. For the highest accuracy, we recommend that you perform this calibration.

Note that this calibration is only effective when radius measurement is enabled by setting the Radius parameter to Display or Yes in the Scan recipe. This means also that the radius measurement should be disabled by setting the Radius parameter to No in the Scan recipe when the instrument is used for other types of measurements.

For maximum precision, the height of the measured arc and the size of the included angle must be within certain limits. These limits depend on the type of measurement head you are using. The height of the measured arc should be limited to 77% of the vertical range of the measurement head, and the included angle to 90°. Measurements can be made up

to 90% of the vertical range of the measurement head in arc height and 110° in included angle with a small loss of precision.

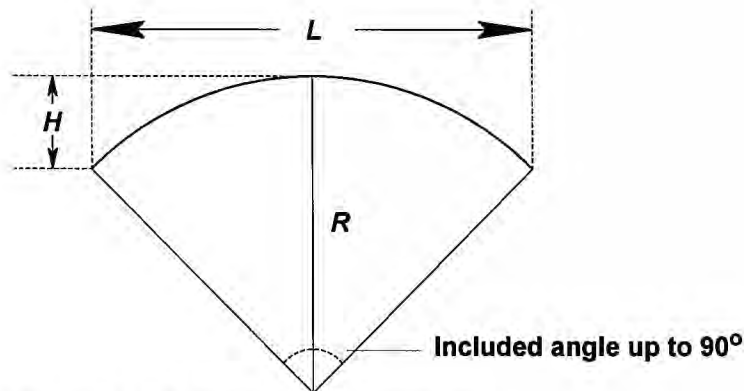


Figure 6-22 Arc Segment Dimensions

Precise measurement is also restricted to arc segments that are symmetric to the radial axis of the measured artifact. To measure another portion of the radius, the sample must be physically rotated about the radial axis.

Scan length and scan speed are dependent on the radius of the sample and the arc height allowed by the measurement head and its vertical range. For a given radius R and optimum arc height H (Fig. 6-22) the optimum scan length L can be determined by the following formula:

$$L = 2\sqrt{2RH - H^2}$$

Scans taken at the lowest possible horizontal resolution for the optimal scan length generally yield the most repeatable and precise radius measurements. To achieve the lowest horizontal resolution, you might have to try various combinations of scan speed and sampling rate. Start with a 200 Hz sampling rate, then set the scan speed to get a scan time that is as close as possible to 25 s without exceeding it. If the longest scan time possible under these restrictions is 12 s or less, set the sampling rate to 100 Hz, and then set the scan speed so that the scan time is as close as possible to 50 s without exceeding it.

Use the center bias profile type if the arc height H is less than about 40–45% of the range available with your measurement head. Otherwise, use either the peak bias (for convex or hill-like radii) or the valley bias (for concave or valley-like radii), as appropriate.

The stylus force needed depends on the arc height H and on the profile type (peak, valley, or center bias). You must set the stylus force high enough for the stylus to reach the lowest points of the scan. If, while measuring a radius, the trace flattens out and no “data out of range” message is displayed, try a higher stylus force setting.

A 1- σ repeatability (precision) of 0.002% of the radius is routinely obtained when you follow a few simple rules:

- Do not use software leveling on the scan data (that is, set both leveling cursors to zero).
- Preset the position of the measurement cursors.

These rules are followed when the Scan recipe is set up as follows:

Recipe Field	Setting
Scan Length	See formula earlier in this section.
Scan Speed	See discussion earlier in this section.
Sample Rate	200 Hz if possible (see discussion earlier in this section).
Surface Parameters	Enable display of Radius and Distance
Stylus Force	See discussion earlier in this section.
Profile Type	See discussion earlier in this section.
Vertical Range	To range necessary to accommodate sample.

Cursors (relative)	Left	Right
Measurement	$L = 2\sqrt{2RH - H^2}$	$L = 2\sqrt{2RH - H^2}$
Leveling	0	0
Delta Meas	0	0
Delta Lev	0	0

For convex radii, the cursors automatically adjust whenever the Edge and Radius parameters are selected in the Scan recipe, and Feature Detection (set for Apex) is enabled.

For 0.002% repeatability, adjust the measurement cursors in the Data Analysis window so that the height values for the cursors are equal within 0.5 μm (20 $\mu\text{in.}$) for radii larger than 2.5 mm (0.1 in.).

6.6 FIT AND LEVEL

The Tencor P-20h software is capable of accurately measuring step heights on curved surfaces (such as lenses or glass optical fibers), or in the case of a bow in a profile that has been leveled in the normal manner. This capability is enabled or disabled in the Scan recipe.

NOTE: The software can remove a simple convex or concave curve from the data, but not more complex curves like waves.

To activate Fit and Level:

Enable the Fit and Level check box in the Feature Detection dialog box of the Recipe Editor.

6.7 SAVING AND MAINTAINING SCAN DATA

Scan data can be saved for reviewing at a later time.

To save scan data:

1. Choose Save Data from the File menu. The following dialog box appears:

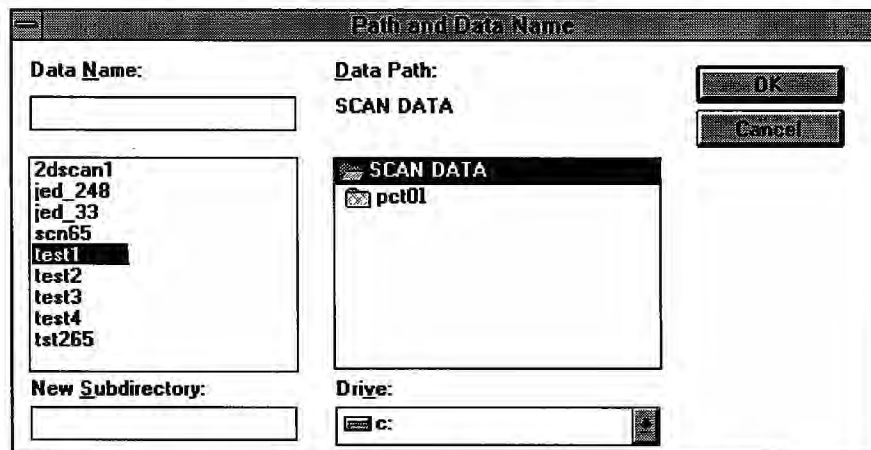


Figure 6-23 Path and Data Name Dialog Box

2. Select the drive and subdirectory.

You can also create a new subdirectory for the new data set by typing a name into the subdirectory field. The new subdirectory then appears in the pathway above the directory window.

3. Type a name for the data set, then click on OK, or click on Cancel to abort the Save operation. The data set name must be a valid DOS filename. Valid DOS filenames
 - Can contain a maximum of eight characters
 - Have a three-character extension supplied by the system
 - Are not case-sensitive

- Can contain only the letters A–Z, the numbers 0–9, and the following special characters: tilde (~), exclamation point (!), at sign (@), number sign (#), dollar sign (\$), percent sign (%), caret (^), ampersand (&), left parenthesis, right parenthesis, underscore (_), hyphen (-), left brace ({), right brace (}), single quotation mark ('), and apostrophe ('). No other special characters are acceptable
 - Cannot be identical to the name of another existing data set
4. Click on OK to enter the path and data name.

Once a data set has been saved, it is added to the Scan Data catalog. The Scan Data catalog window allows you to select individual data sets for reviewing. You can also delete unwanted data sets.

To view the Data catalog:

From the Catalog window, click on the Scan Data button on the left side of the screen. The Scan Data Catalog window appears:

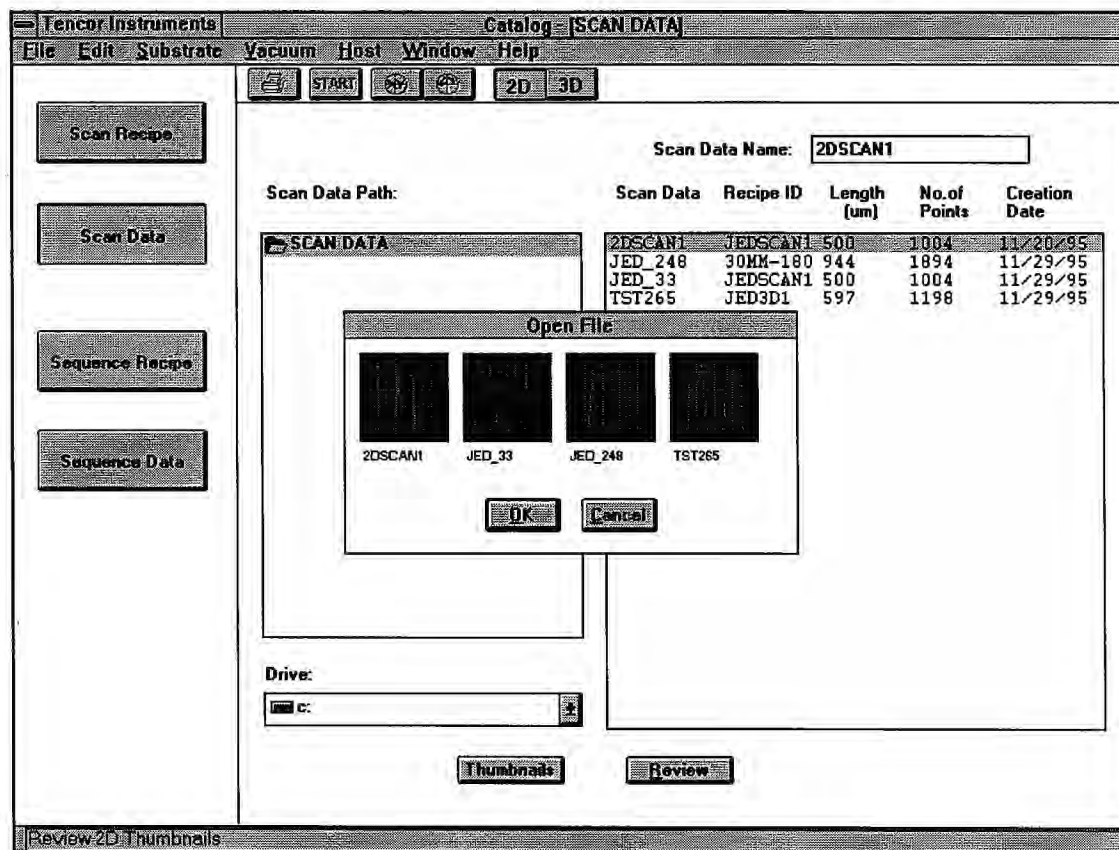


Figure 6-24 Scan Data Catalog Window

To review a data set:

Select the desired data set from the list in the catalog, and click on the Review button, or double-click on the desired data set.

To delete, import, and export data, see Chapter 9, “Using the Database.”

7 ANALYZING 3D SCAN DATA

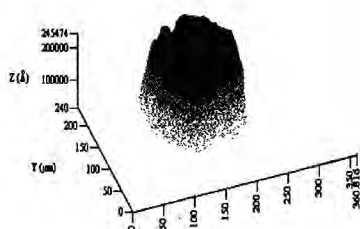
Once a 3D scan has been completed, the computer processes the measurement data and displays it in the Data Analysis window. This chapter discusses how data from a 3D scan is displayed and how to manipulate and analyze it.

This chapter describes

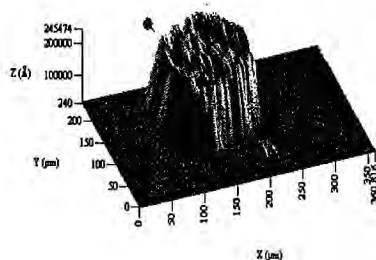
- Parts of the 3D Data Analysis Window
- How to customize images
- How to analyze 3D data
- Leveling the data

7.1 DATA ANALYSIS WINDOW

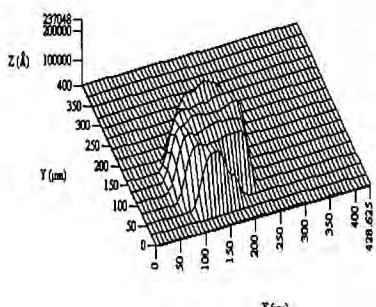
When a scan is completed, the Data Analysis window appears, showing a three-dimensional, color representation of the data points collected in one of three selectable formats:



By Height: the higher the feature, the lighter the color. Good for viewing rough features.



By Light: features appear as if illuminated by a light source. Good for viewing smooth features since contours are more obvious.



By Line: only the data points are plotted, giving a wire frame effect. Unlike the other two formats, it does not “fill in” between the scan lines with interpolated data to create the look of a solid object. Good for viewing surface detail.

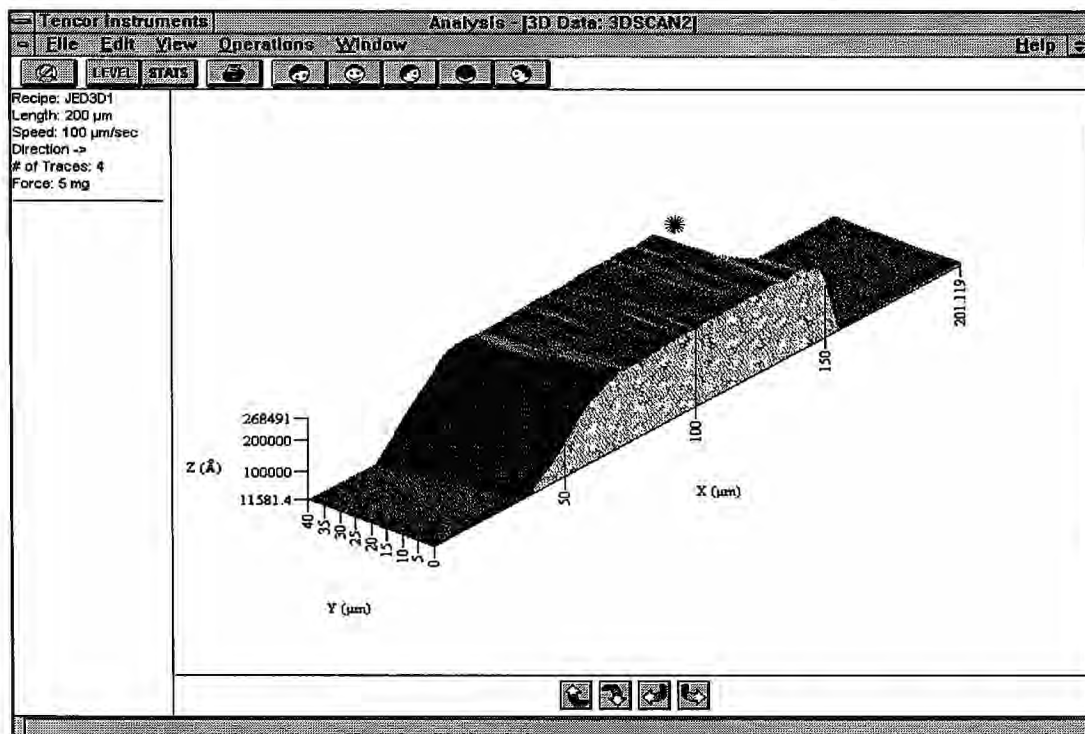


Figure 7-1 Data Analysis Window, image displayed in By Light format

7.1.1 DATA ANALYSIS MENU BAR

Most of the data manipulation and analysis of 3D scans is performed using either the 2-D view of the 3D scan or a single XY trace that you select from the 3D scan. Therefore, many of the tools you use for 2D data analysis you will use with 3D scan data.

The menu bar for 3D analysis adds the following two menus for operations specific to 3-D data manipulation:

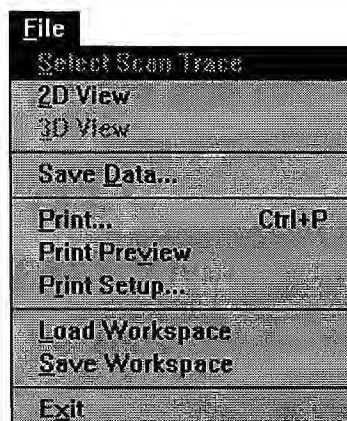


Figure 7-2 File Menu

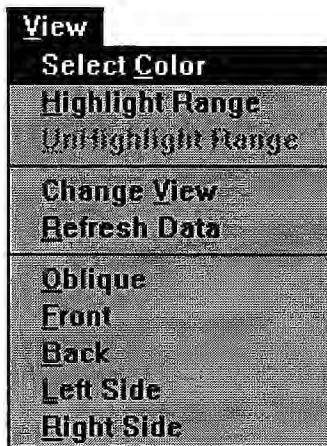


Figure 7-3 View Menu

7.1.2 DATA ANALYSIS TOOL BAR

The Data Analysis tool bar contains 3D image orientation buttons that provide a quick alternative to changing the view angle of the scan using the View menu and Rotation buttons

Clicking on **displays the image as if you are**



in front and to the left of the scan.



in front of the scan.



in front and to the right of the scan.



in back of the scan.



at the end of the scan.

You can also use the Rotate Arrows at the bottom of the 3D View window to obtain more customized views.



7.1.3 GRAPHICS TOOLS

These tools, located at the far right of the menu bar, are active when the 2D view of the 3D scan is selected.



Zoom In—Allows you to scale up a selected feature.



Undo Zoom—Returns the scan view to the original scale.



Ruler—Allows you to select a single scan trace for 2D display and data analysis.



Level—Allows you to level a 3D scan.



Height Tool—use to measure the height of a specific area on the scan.



Step Height—use to designate two areas on the scan for step height measurement.

7.2 CUSTOMIZING THE SCAN IMAGE

Z determines the relative height of the scan in relation to the X and Y axes, allowing you to customize image proportions.

To set image proportions:

1. Select Change View from the View menu. The Set 3D View Parameters dialog box appears.
2. Type a number that gives a satisfactory height to the image. Since the number depends on the relative heights of the features in the image, choose a higher value to obtain a taller image, a smaller value to reduce it.
3. Click OK to close the dialog box and apply your choice.

The computer records more data points than are possible to plot onscreen, so it uses a subset of the points taken to build the image. In general, the smaller the subset, the coarser the image and the faster it can be displayed and rotated. You can control the image granularity from coarse to fine by setting parameters for the data subset. For instance, a setting of 3 plots every third data point and represents a subset one-third the size of the original data set.

To set x and y granularity:

1. Select Change View from the View menu. The Set 3D View Parameters dialog box appears.
2. Type a number in either or both X and Y granularity fields. A larger number than the currently displayed value increases granularity; a smaller number decreases it.
3. Click OK to close the dialog box and apply your choice.

You can customize your 3D data images to better represent your substrate type by selecting a shading mode. Choose By Lines for a wire frame effect, By Height to emphasize high features, and By Light to enhance smooth surfaces.

To select the shading mode:

1. Select Change View from the View menu. The Set 3D View Parameters dialog box appears.
2. Select By Lines, By Height, or By Light.

If you choose By Light, you can optimize its effect by changing the position of the light source:

In the box below the Shading Mode, enter Rise and Rotation angles from 1° to 90°. The reference point for these angles is an imaginary center located on the X-axis halfway down its length. The numbers you enter represent locations clockwise and up from this point.

3. Click OK to close the dialog box and apply your choice.

To change your angle of view:

You can view the image from various angles using four different features:

Orientation selections on the View menu: Select the View menu and click on one of the five views listed at the end of the menu.

Orientation tool bar: Click on the face icon corresponding to the desired angle. Also, clicking one of these buttons returns you quickly to 3D view from 2D views.

View Vector Settings—choosing a specific angle of view:

1. Select Change View from the View menu.

2. Enter angles for the desired viewpoint in the data entry fields.

The Rise setting rotates the image around its X-axis. Entering a 90° rise setting stands the image on edge, giving a top-down view; a 45° rise tilts the far side of the image away from you. See Figure 7-4.

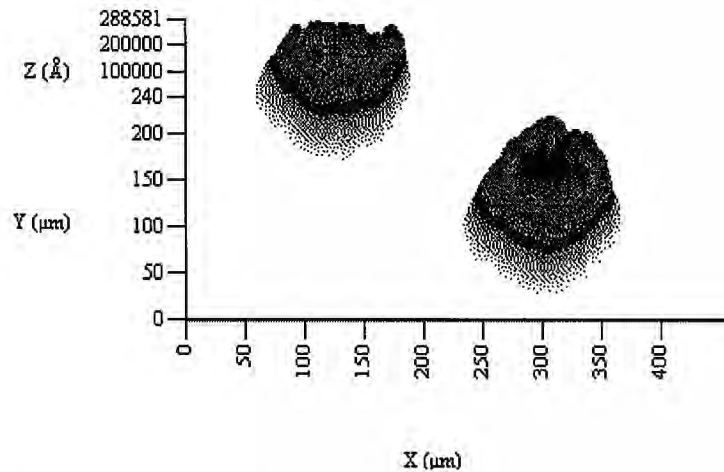


Figure 7-4 View Vector Settings: Rise 45 °, Rotation 0°

The Rotation setting pivots the image counterclockwise on its XY plane. A 0° rotation aligns the X and Y axes with the window frame in a straight-on side view (Figure 7-5); 45 ° rotates the image to lie diagonally across the window. You can even enter rotations up to 359 ° to rotate the image completely around to the “back” side. Figure 7-6 shows the image at 45° rise and 45 ° rotation.

3. Click OK to close the dialog box and apply your choice.

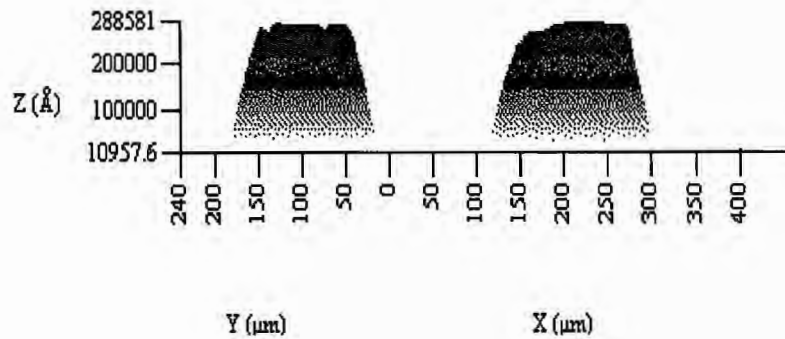


Figure 7-5 View Vector Settings: Rise 0°, Rotation 45 °

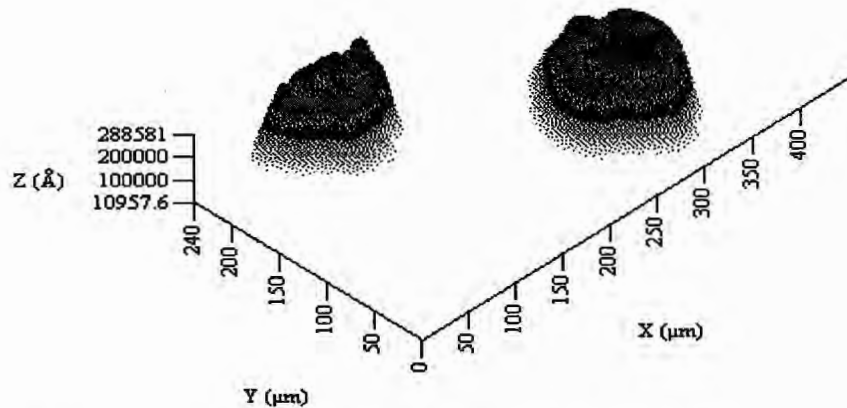


Figure 7-6 View Vector Settings: Rise 45 °, Rotation 45 °

Rotation Tools

The rotation tools at the bottom of the 3D view window give you a quick way to examine the image from continuously changing points of view.

You can choose from a palette of 42 basic colors for your images or mix your own from the custom paintbox.

To customize image colors:

1. Choose Select Colors from the View menu.
2. Click on the desired color or on Define Custom Color if you want to mix your own. Saving the scan file also saves custom colors.
3. Click OK to close the dialog box and apply your choice.

You can color-code images displayed in the By Height format to better delineate height features. The Highlight Ranges feature lets you assign different colors for different height ranges, giving a topographical representation of the substrate.

To color-code the scan for height:

1. Select Highlight Ranges from the View menu. A dialog box appears, giving the minimum and maximum heights obtained in the scan and two parameter entry fields.
2. In the range top and bottom entry fields, type values for the top and bottom boundaries of the height range.
3. Click Select Highlight color.
4. Choose a color from the palette or mix your own.
5. Click OK. The Highlight Height Range dialog box reappears.
6. Repeat for as many ranges as you want to define.
7. Click OK to enter the parameters and apply the ranges to the scan.

You can set the image to automatically expand to the largest size the window allows.

To size the image to fill the window:

1. From the View menu, select Change View
2. Click on the box next to "Maximize image to fit window," at the bottom of the dialog box.

To deactivate the maximize option, click on the box again to uncheck it.

You can display any or all open windows, including the 3D scan and the 2D trace you select from it.

To view 2D traces and 3D scans at the same time:

1. To display a single trace from the 3D scan:
 - From the 3D scan, choose 2D View from the File menu. The 3D image rotates to an XY, top-down viewpoint and the Graphics tool bar appears in the menu bar.
 - Click on the Zoom In tool. A framed box appears on the scan.
 - Click and drag across the area you want to select. Use the magnifying crosshair to locate your starting and end points.

- Choose Select 2D Trace from the File menu to open a new window displaying the single trace in XY view.
- 2. To open multiple windows, choose a tile selection from the Windows menu. Tile Horizontal usually works best.

7.3 ANALYZING SELECTED FEATURES

Viewing a particular feature in a 3D scan requires that you display it in 2D View.

To zoom in, 3D View:

1. Choose 2D View from the File Menu.
2. Click on the Zoom In button on the Graphics tool bar on the right side of the menu bar.
3. Click and drag to draw a box around the feature you want to enlarge.

When you release the button, the feature appears, full size, with axes rescaled in proportion.

To zoom in, 2D Trace:

1. From a 2D trace view, click the Zoom In button on the *left* of the menu bar. The zoom tools on the Graphics tool bar on the right are active only for 3D scans.
2. Position the arrow cursor on the scan and click and drag from one side of the desired scan segment to the other. Vertical cursor lines appear, one on each end of the segment.
3. Release the trackball button. The scan rescales to display only the selected segment.

To undo zoom:

There are two ways to return to the original scan magnification:

- Use the Undo Zoom tool on the left side of the tool bar for 2D Traces. Use the Undo Zoom tool on the Graphics tool bar for 2D Views of 3D scans (See the following note for an explanation of 2D Traces and 2D Views). These icon buttons reduce magnification in steps back to the original scale. Click on the button until the feature zooms out to the desired scale.
- To return in one operation to the original scan scale, select Undo Zoom from the Operations menu.

7.4 DATA LEVELING AND MEASUREMENT

Data leveling and measurement is performed from the 2D view of the 3D scan using the Graphics tool bar.

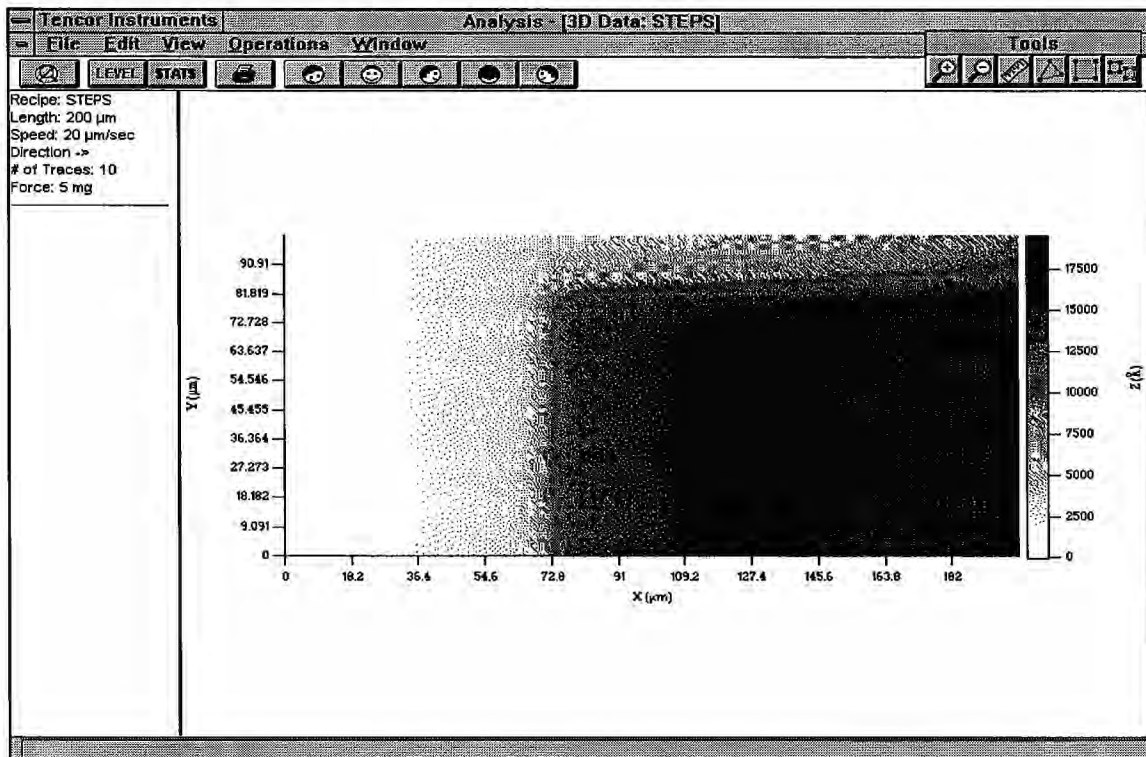


Figure 7-7 2D View of a 3D Scan

NOTE: 2D View and 2D Trace refer to different representations of 3D scan data. A window displaying a **2D View** is actually the 3D scan as it appears from directly above, from the top down. In this view, scan features appear flat, their shapes indicated by gradations of color. To provide a quantitative indicator of height (the Z scale), the 2D View screen includes a ruled strip beside the scan window color-keyed to indicate the range of heights in the scan (Fig. 7-7). Displaying a 2D View requires the selection of the 2D View from the File menu.

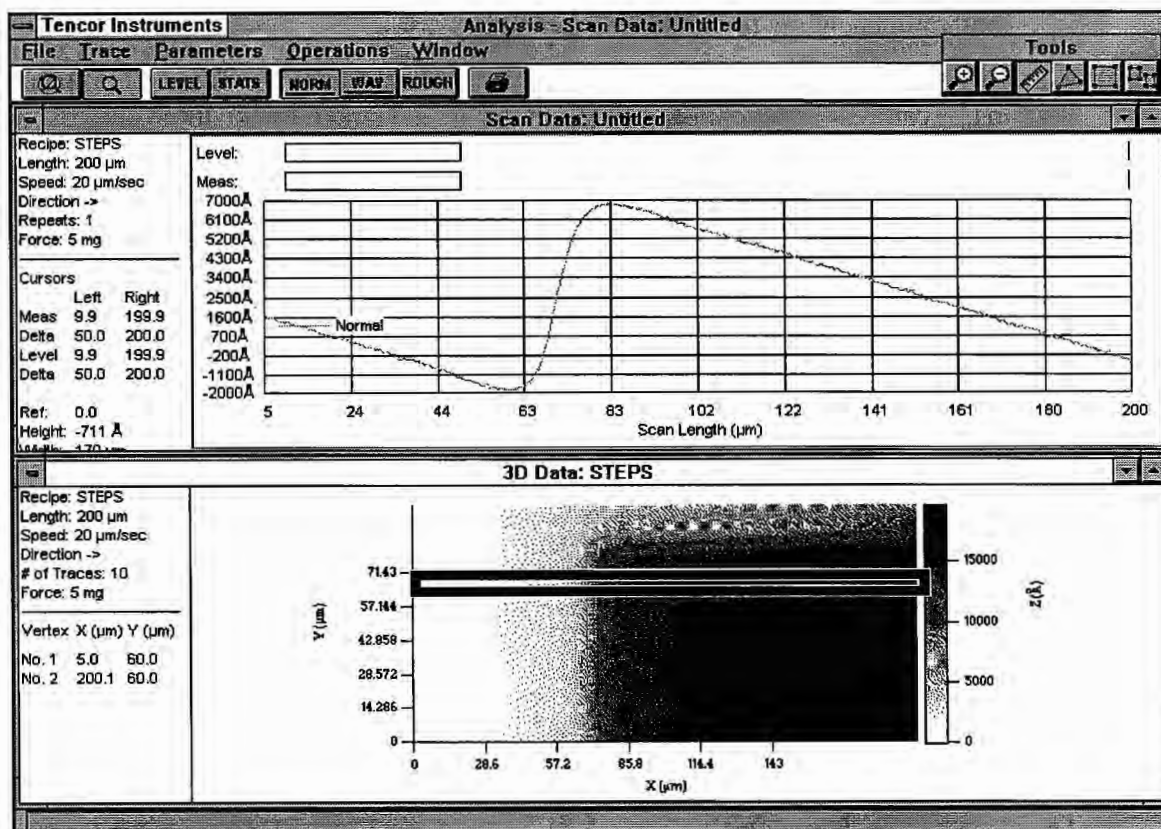


Figure 7-8 A 2D Trace (top window) from the selected trace of the 2D View (bottom window)

On the other hand, a **2D Trace** is an actual XY plot of one of the traces comprising the 3-D scan. Onscreen, it looks like a 2D scan, and you can perform data analysis on it just as you would for a 2D scan. From the 2D View of the 3D scan (described above) you select which scan to display using the ruler on the Graphics tool bar. To display the trace, you choose Select Trace Scan from the File menu (Fig. 7-2).

7.4.1 DATA LEVELING

Software data leveling of 3D scan data is much the same as for 2D scan data (Section 6.2, "Data Leveling and Measurement"). However, 3D data leveling must allow for an additional spatial dimension, so it is performed using three leveling cursors.

To level data:

1. Select 2D View from the File menu. The screen shows the 3D scan from the top down.
2. Click on the Leveling Triangle on the Graphics tool menu bar.
3. Position the arrow on the scan and click to place the first of three cursors. A small box marked "1" appears, forming the first vertex of the leveling triangle.

4. Repeat this step to set the other two cursors of the leveling triangle.
You can also click and drag between cursors. To change the cursor positions, click and drag each one to the desired position.
5. Click on the Level button in the tool bar or select Level from the Operations menu.
The scan will be leveled according to the areas marked by the three cursors (not the connecting lines).
6. To record the positions of the level cursor in the scan recipe, select Recalc from the Operations menu.

7.4.2 USING 3D SCANS FOR 2D DATA ANALYSIS

1. From the 3D scan, choose 2D View from the File menu. The 3D image changes to a top-down view and the Graphics tool bar becomes active.
2. Click on the Zoom In tool. A framed box appears on the scan.
3. Click and drag across the area you want to select. Use the magnifying crosshair to more precisely locate your starting and end points.
4. Choose Select 2D Trace from the File menu to open a new window displaying the single trace in XY view.

7.4.3 MEASUREMENT

To measure average height:

1. Choose 2D View from the File menu. The scan appears as viewed from the top down.
2. Click on the ruler tool of the Graphics tool bar to activate the measurement cursor.
3. Position the arrow at the starting point of the feature you wish to measure.
4. Click and drag to the endpoint of your measurement. The arrow becomes an enlarged crosshair that magnifies the detail of the underlying area, which allows you to more precisely set your starting and end points. A framed box marks the length of the measurement along the X axis.

Measurement values appear in the Trace Information area to the left of the scan.

5. To record the positions of the level cursor in the scan recipe, select Recalc from the Operations menu.

To measure step height:

1. Choose 2D View from the File menu.
2. Click on the Step Height tool of the Graphics tool bar to activate the measurement cursor.
3. Position the cursor arrow near an area you wish to include in the measurement.
4. Click and drag the box around the area. Release the button.

5. In the same manner, draw another box around the area you wish to compare it to. The measured values and box parameters appear to the right of the scan.
6. To record the positions of the level cursor in the scan recipe, select Recalc from the Operations menu.

7.5 X START LEVELING

X Start Leveling is a 3D scan parameter option found in 3D scan recipes that starts the beginning of each successive scan at the same height. Using X Start Leveling removes bow from the scan, makes surface features stand out, and helps to reduce the effects of mechanical noise.

1. Open the recipe for the scan, or create a new one (see Section 4.2, "Recipe Editor Window").
2. Check the box beside the words, "X Start Level."
3. Click OK to close the dialog box and apply your selections.

8 SEQUENCING

The Tencor P-20h allows you to write a *sequence*, which instructs the instrument to take a series of scans rather than you taking them all manually one by one. A sequence is like a script that links specific scan sites on a sample (or on a number of samples) with specific scan recipes to be performed at each site. The capability of automating repetitive measurements greatly enhances the productivity of the instrument.

This chapter covers

- Sequencing capabilities of the P-20h
- The Sequence Editor window
- Sequence Editor fields
- A simple sequence example
- Sequencing with Manual Deskew and Pattern Recognition Deskew
- Sort options
- Sequencing with the wafer handler
- Saving and maintaining sequences, and printing sequence data

8.1 SEQUENCING CAPABILITIES

The Sequencing provides the following measurement capabilities:

- Combine as many artifact sites and recipes as desired
- Set reference points for correcting for translational and rotational variation between wafers (deskew)
- Deskew can be set manually or automatically using Pattern Recognition
- Set Pattern Recognition options to search locally for a match when a match is not found in the camera's field of view at deskew sites and carry out user-selected instructions if the search fails
- Set the wafer handler to load, scan, and unload up to 26 wafers without operator intervention
- In Multiple Analysis mode, apply different recipes to a single scan
- Automatically display, print, export and save statistics or raw data for all sites
- Teach scan sites and alignment reference points interactively, with or without theta
- Unload wafers that do not meet pass/fail criteria into a designated cassette

8.2 SEQUENCE EDITOR WINDOW

The Sequence Editor window contains the controls for writing and editing sequence programs, setting various sequence options, and running the sequence program. The Sequence Editor is started from the Sequence Recipe Catalog. (See Section 4.1.1, "Scan Recipe Catalog Menu Bar," and Section 4.1.2, "Scan Recipe Catalog Tool Bar," for a description of the menus and tool bar buttons that appear in the Sequence Recipe Catalog window.)

To view the Sequence Editor window:

1. From the Top Level menu, double-click on the Scan icon. The Sequence Recipe Catalog window appears:

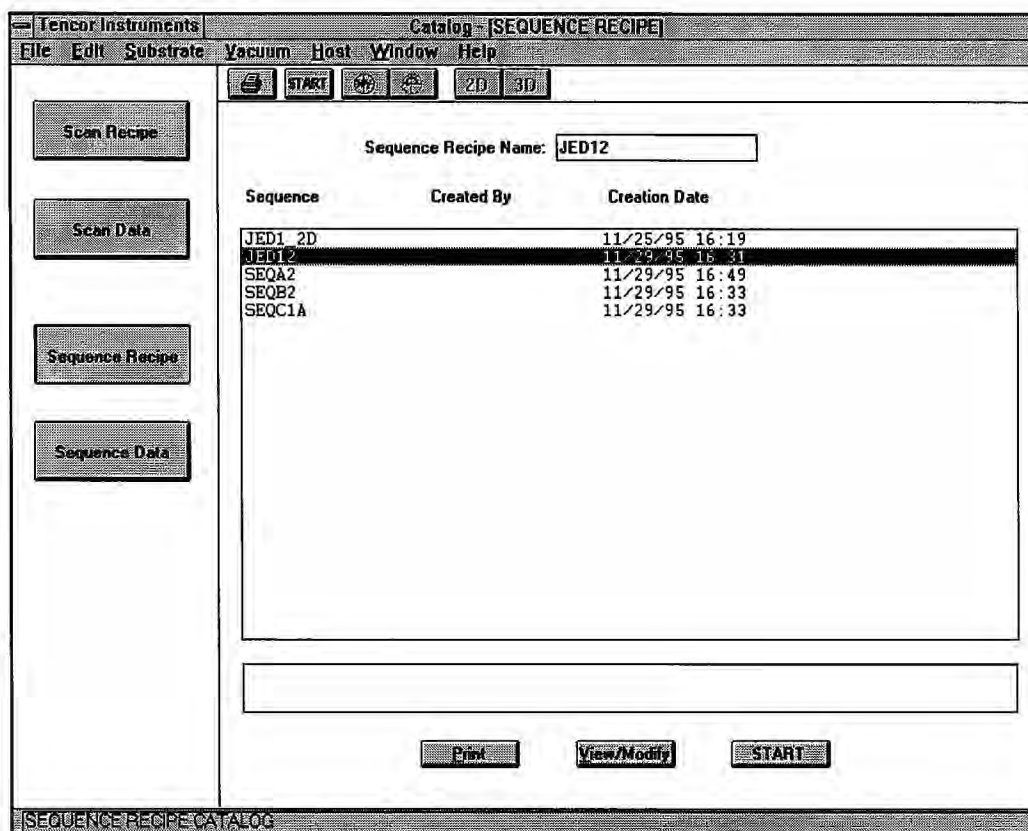


Figure 8-1 Sequence Recipe Catalog Window

2. Click on the View/Modify button below the list of sequence recipes, or double-click on any of the sequence recipes in the list. The Sequence Editor window appears (Fig. 8-2).

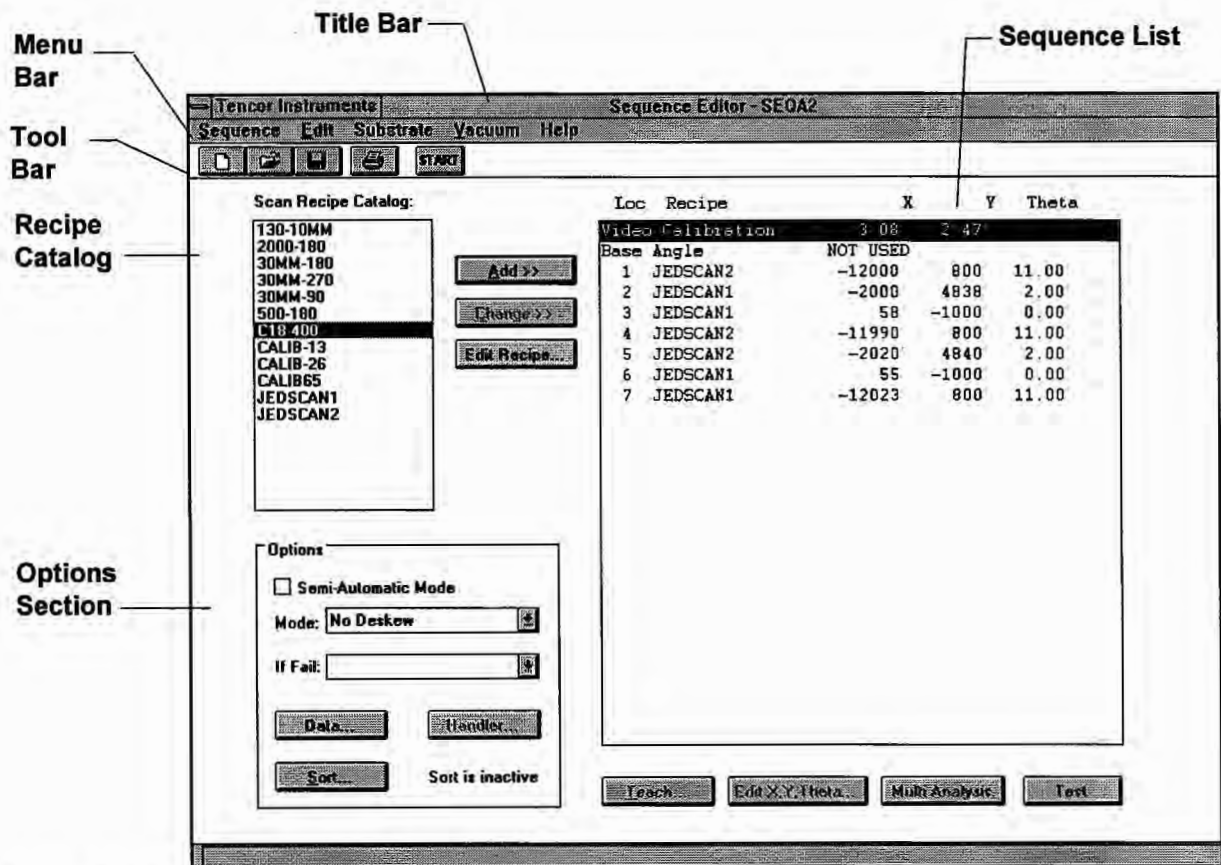


Figure 8-2 Sequence Editor Window

The Sequence Editor window consists of the following elements:

- Menu bar
- Tool bar
- Recipe catalog for selecting from available recipes
- Options section for setting sequence options
- Control buttons for sequence programming
- Sequence list, linking sites with recipes

8.2.1 SEQUENCE EDITOR MENU BAR

The Sequence Editor menu bar provides access to commands through its menus. You can view menus by clicking on the titles in the menu bar, or by pressing ALT+*l*, where *l* is the letter that appears with an underscore in the desired title in the menu bar. You can choose menu items by clicking on a menu entry or by typing the letter that appears with an underscore in the desired menu item.

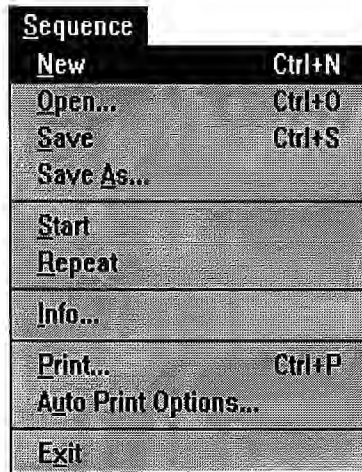


Figure 8-3 Sequence Menu

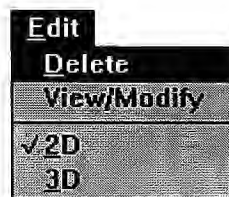


Figure 8-4 Edit Menu

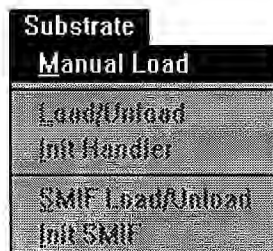


Figure 8-5 Substrate Menu








Figure 8-6 Vacuum Menu

8.2.2 SEQUENCE EDITOR TOOL BAR

The Sequence Editor tool bar contains a row of icons that resemble buttons. Clicking on these icons provides an alternative way to access commonly used functions.

Each icon suggests the function of the button. For example, the Print button resembles a printer. Buttons that appear dimmed are unavailable.

The Sequence Editor tool bar contains the following buttons:

Button	Action
	Loads a new default sequence
	Displays the File Open dialog box
	Saves the current sequence
	Displays the Print dialog box
	Starts a scan using the current Sequence

8.2.3 SEQUENCE INFORMATION DIALOG BOX

The Sequence Information dialog box displays the title, author, the date and time of creation (or modification) of the sequence, and a section for annotating the sequence with comments.

To display the Sequence Information dialog box:

Choose Info from the Sequence menu.

The Sequence Info dialog box also appears when you are saving a sequence.

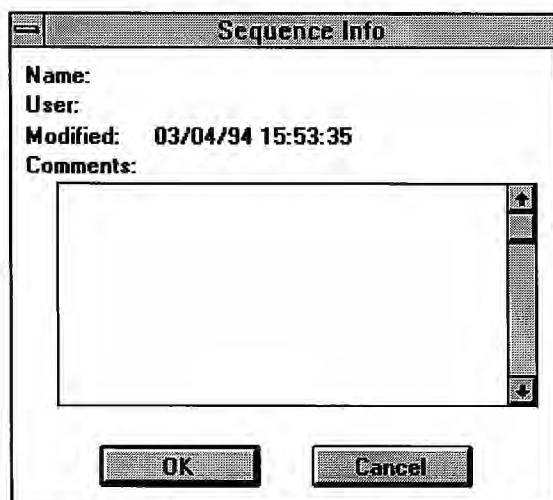


Figure 8-7 Sequence Information Dialog Box

The Name, User, and Modified fields are supplied automatically by the system. These fields cannot be edited.

To enter Comments:

1. Click in the Comments text box or press TAB← or TAB→ until the Comments text box is highlighted.
2. Type the desired text.

8.2.4 SEQUENCE EDITOR RECIPE CATALOG

The Sequence Editor Recipe catalog is a list box for displaying and selecting recipes. It has a vertical scroll bar to allow display of all currently available stored recipes.

To select a recipe:

Locate the desired recipe name. If the name is not visible in the window, use the scroll bar to find it, or click on any of the recipe names and then press [^] or [v] to move the selection bar up or down.

Note: Sequencing is not currently available for 3D scans.

8.2.5 OPTIONS

The Options section allows selecting the sequence mode and setting the Data, Handler, and Sort options for the sequence. You can also select to run the sequence in Semi-Automatic mode.

SEMI-AUTOMATIC MODE

The Semi-Automatic mode causes a sequence to display the trace data after each scan and pause before proceeding to the next step. Each step can be verified and, if needed, the scan sites can be adjusted and the scan retaken before proceeding to the next step. In Pattern Rec. Deskew mode, you can manually adjust the position of the stage in case the deskew site does not appear in the field of view when the sequence begins.

Enable the Semi-Automatic mode by clicking on the check box. An X in the check box indicates that the Semi-Automatic mode is enabled; a clear check box indicates it is disabled.

Mode

Select the Sequence mode from the drop-down list. The available modes are

No Deskew	The sequence contains no deskew points for alignment.
Manual Deskew	Sequence deskew points are set much like scan sites.
Pattern Rec. Deskew	Sequence deskew points are set using the Pattern Recognition option.

Fail Options

Select the action you want taken if pattern recognition fails to find a deskew point. Fail options are

Proceed Measurement	Continue with the scanning sequence.
Skip, No Measurement	Measurement of that wafer is suspended.
Retry Pat. Rec. Manually	Allows user to perform a manual deskew.
Cancel Sequence	Sequence is suspended. User must restart.

DATA OPTIONS DIALOG BOX

Set the Data options by clicking on the Data Options button in the bottom of the Options dialog box. The Data Options dialog box appears:

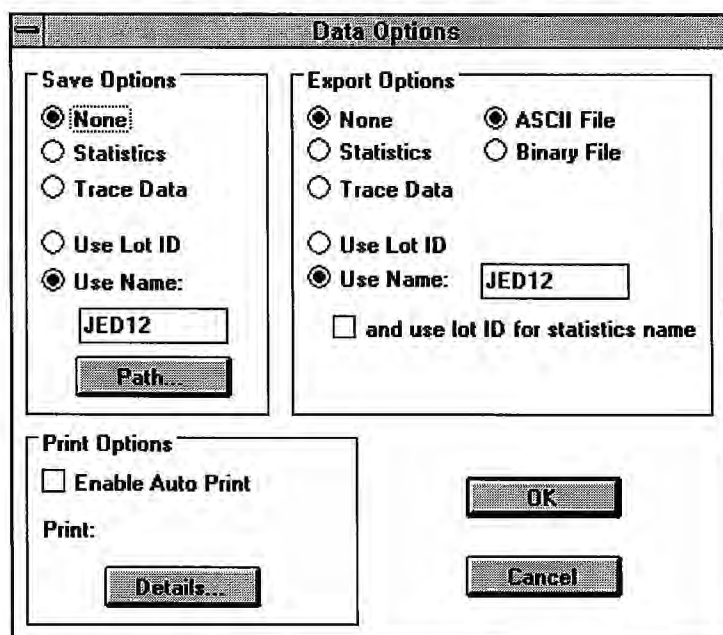


Figure 8-8 Data Options Dialog Box

Make a selection from Print, Save, and Export options, click on the appropriate radio button. When finished, click on OK to set the options and close the dialog box, or Cancel to close the dialog box without changing the previous settings.

Each group has the following possible settings:

None	Prints, saves, or exports no data.
Statistics	Prints, saves, or exports only the statistics for the specified parameters, the recipe ID, part ID, and sequence ID. The results for each parameter at each measurement site are not printed, saved, or exported. Statistics are calculated for scans taken with the same recipe and are saved only if two or more scans are taken with that recipe. For information on the Combined Sequence Statistics Option, see the Section 8.15, "Combined Sequence Statistics (Optional)," following.
Trace Data	Prints, saves, or exports everything, including the recipes used, the raw data points for each scan, parameter results, and the statistics.

The Export Options also contain a choice of export file type:

ASCII File Data is exported in ASCII representation.

Binary File Data is exported in binary representation.

HANDLER OPTIONS DIALOG BOX

Set the Handler options by clicking on the Handler Options button at the bottom of the Options dialog box. This displays the Handler Options dialog box (Fig. 8-23).

The settings under the Handler Options dialog box are described in Section 8.12, "Sequencing with the Wafer Handler."

SORT OPTIONS DIALOG BOX

Set statistical pass/fail criteria for each recipe by clicking on the Sort button in the Options dialog box. Besides data entry fields for minimum and maximum data point, mean, standard deviation and range, the Sort Options window lists the corresponding values from the previous scan to provide a side-by-side reference for setting values. From this dialog box, you also can choose to include failed slots in the cassette summary.

8.3 WRITING A SEQUENCE

This section covers the basic outline of a sequence. The sections that follow discuss in more detail some of the operations outlined in this section.

Note: Sequencing is not currently available for 3D scans.

The steps in writing a sequence need not follow a specific order, except for the following:

- The Sequence Editor needs to be opened first.
- The sequence sites must be taught before the sequence can be saved.

All steps may not be necessary. For example, you may not need to edit the sequence.

To write a sequence:

1. Open the Sequence Editor by choosing View/Modify from the main Scan window. You can start a new sequence by choosing New from the Sequence menu, or edit an existing sequence by choosing Open from the Sequence menu and selecting the desired sequence from the dialog box.
2. Add the desired recipes to the sequence list on the right side of the window by selecting a desired recipe and clicking on the Add>> button.
3. Set the desired options. Enable or disable Semi-Automatic mode, select the Sequence mode, set the Data Options for saving, printing, and exporting data, and set the Sort and Handler Options if needed.
4. Load a wafer or sample.

5. Teach the Base Angle if used.
6. Teach the sequence sites. If Deskew is used, teach the two Deskew Sites first, then the steps.
7. Edit the sites if needed. Select the desired site and click on the Edit X,Y, Theta button. Or, manually enter or modify the coordinates.
8. Save the sequence by selecting Save As from the Sequence menu.

To run a sequence:

- Start the sequence by clicking on the Start button in the tool bar, or choosing Start from the Sequence menu.

To stop a sequence:

- Stop the sequence by clicking on the Stop Scan button in the Scan window. The handler automatically unloads the wafer.

8.4 A SIMPLE SEQUENCE EXAMPLE

This section provides a brief tutorial example describing the process of writing, setting up, and running a simple sequence on a single sample without deskew and without the handler.

The example used throughout this tutorial follows a continuous sequence of steps. By carefully following the instructions, the windows that appear on your screen should be very similar to the example windows reproduced in this chapter.

To work through this section, you will need

- A sample to profile
- One or more recipes

We recommend a step-height standard for this purpose. You can use any recipe and modify it as you proceed.

To write the sequence:

1. Bring up the Sequence Editor window (Fig. 8-2) by choosing View/Modify from the Sequence menu of the Scan Application window.
2. To make sure you begin with a blank sequence, choose New from the Sequence menu. Two entries, Video Calibration and Base Angle, appear in the sequence list on the right side of the window. The mode is set as No Deskew and the Data, Handler, and Sort options are set to their defaults. A Video Calibration step appears at the beginning of every sequence to assure accurate results for scan length teaching and for pattern recognition. It is only necessary if the optical magnification (zoom) has been changed. Base Angle is an offset angle relative to the wafer's flat or notch.
3. Select one of the designated recipes in the Recipe Catalog list box.

4. Click on the Add button, or press ENTER. The name of the selected recipe appears as site 1 in the sequence list.
5. Select another one of the designated recipes in the Recipe Catalog list box, or use the same one again, and add it to the sequence list in the same way.
6. Add one more recipe to the sequence list in the same way. You now have three sites in the sequence list, each of which uses the chosen recipe(s) to control the scan and calculate the results for that site. Next, you need to specify X and Y coordinates to each site (θ coordinates are only necessary if a stage rotation is incorporated into a sequence).
7. Select the first site by clicking anywhere on the site 1 line in the sequence list, or use [^] and [v] to move the selection bar to site 1.
8. Click on the Teach control button, or double-click on the selected sequence step. The Teach Location window appears:

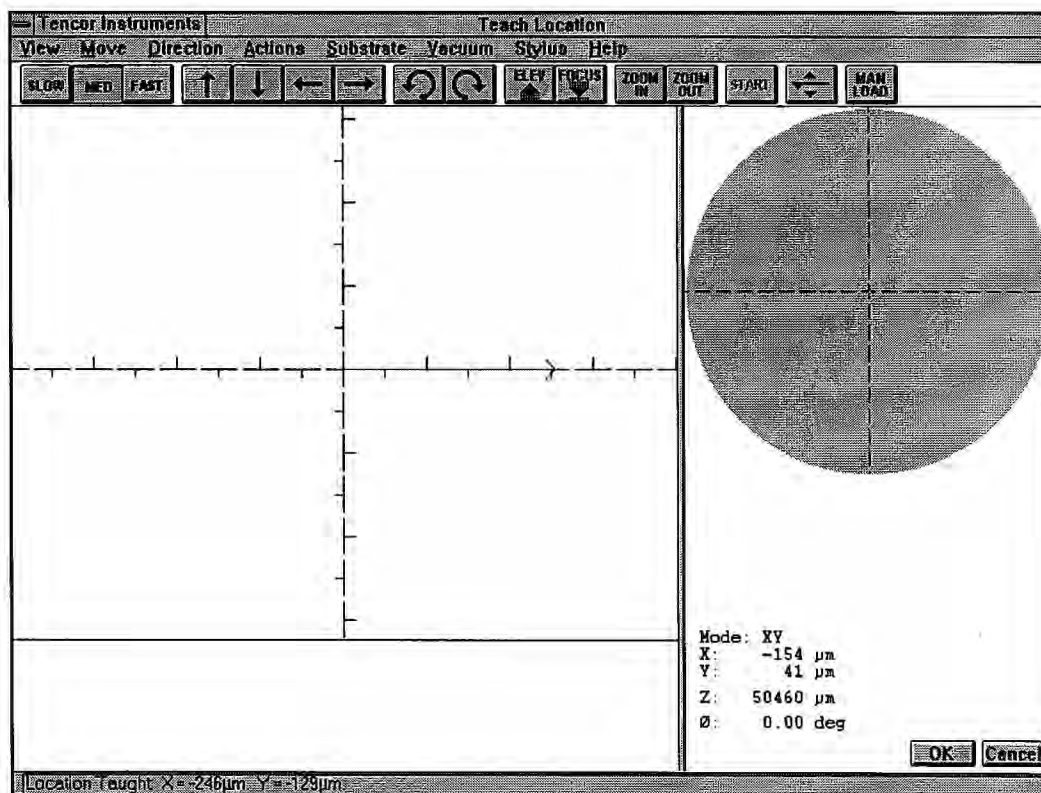


Figure 8-9 Teach Location Window

9. In the Teach Location window, the blue arrow superimposed on the cross hairs indicates the scan length and direction as defined in the recipe. The center of the cross hairs indicates the start-of-scan position. Locate an appropriate position to start a scan as follows:
 - Move the stage using the arrow buttons in the tool bar, or clicking in the round stage position control on the right of the video window.
 - When the desired feature is in the field of view, indicate the position to start the scan by clicking there on the video image.
10. Click on OK, or press ENTER, to return to the Sequence Editor window. Note that the X and Y coordinates of the cross hair now appear to the right of the recipe name in the sequence step for site 1.
11. Repeat the teach process for each of the other sites in the sequence list, moving to a different place on the sample for each. When you are finished, you should have a sequence list with the following lines: the optional Video Calibration step, the Base Angle step (not used here), and three scan sites with specific recipes and X and Y coordinates.
12. Save the sequence by selecting Save As from the Sequence menu.

To run the sequence:

Start the sequence by selecting Start from the Sequence menu, or by clicking on the Start button in the tool bar.

The Run application window appears, and the stage moves to the first site. The stylus descends to the sample surface and the first scan begins. When the scan is complete, the stylus lifts, the stage moves to site 2, and the second scan begins. When this scan is complete, the stage moves to site 3 and the third and final scan begins.

At the end of the final scan, the stage returns to its initial position and the Scan Trace window appears. Choosing Sequence List from the File menu displays the Data Analysis window. Both windows can be resized, moved, minimized or maximized, as well as tiled for simultaneous display (Fig. 8-10) and the screen arrangement saved. See Section 2.6.9, "Moveable and Resizeable Windows."

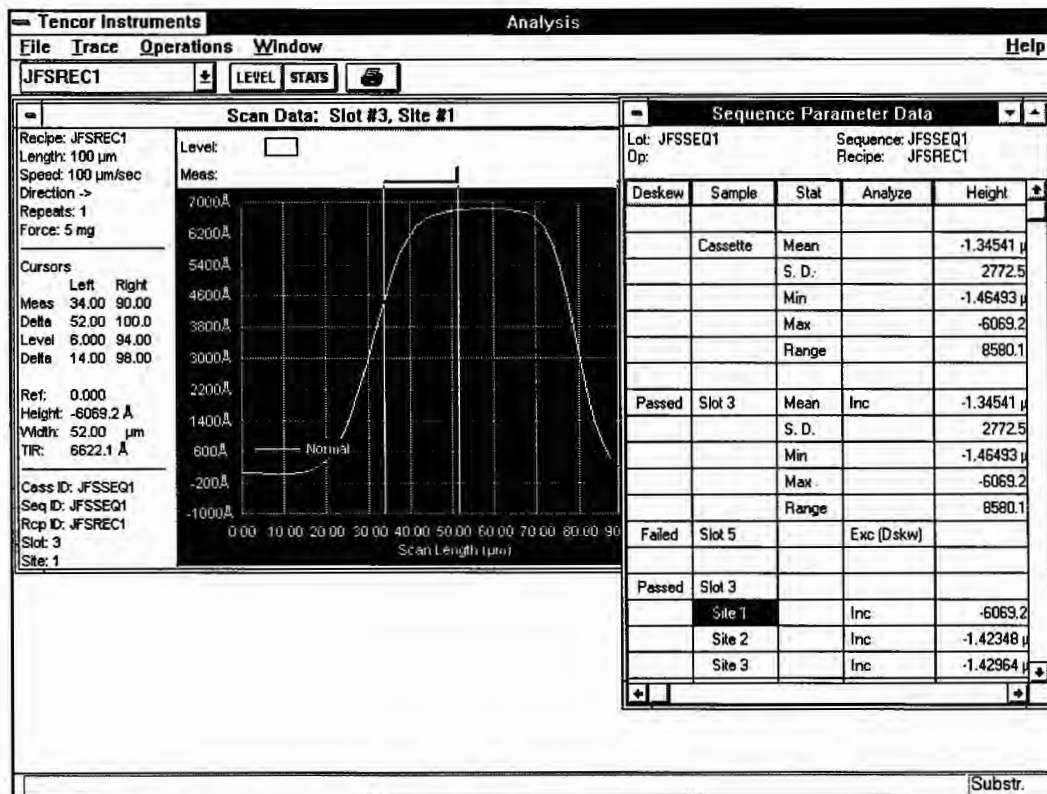


Figure 8-10 Sequence Data Analysis Window

8.5 MULTIPLE ANALYSIS

You can obtain multiple data analyses from a single scan by applying the data analysis settings of additional recipes to its raw data. The process is a modification of a sequence recipe in which the instrument uses the first scan recipe to scan and analyze in the usual manner, then takes settings from the subsequent recipes to reanalyze the first recipe's scan data.

You can save time and improve throughput by using multiple analysis for

- Measurements that require more than one cursor setting, for example, two different step heights on a single scan
- Measurements with different filter settings
- Measurements with different surface parameters enabled in the recipe

To create a multiple analysis recipe and scan the sample:

1. From the Sequence Recipe catalog window, click on a recipe, then View/Modify to open the Recipe Editor window.
2. Select New from the Sequence menu. A blank sequence list appears.
3. Set up the scanning recipe:
 - If you plan to scan with a recipe's existing settings, click on the name of the recipe you wish to scan with and add it to the list.
 - If you want to make changes to the recipe, click on its name in the list, then on Edit/Review to change any parameters and teach the cursor position.

Note: If you want to teach cursor positions later from the scan trace, you must perform a Save As to create a new recipe—even if you make no changes to the recipe at this point.

After saving the recipe, exit the Recipe Editor to return to the Sequence Editor window.

Select the new recipe you just created.

Click on Change to replace the original recipe (still highlighted) with the new recipe in the list.

4. Set up the analyzing recipes:
 - From the recipe catalog list, click on a recipe containing the analysis settings you want. This recipe should have the same scan length, scan speed, sampling frequency, stylus force, contact speed, and range as the scanning recipe.
 - Make changes to the recipe as in step 3. You can also perform this step before compiling the sequence list, using the recipe to scan the sample and teach the cursor positions.
 - Add the recipe to the sequence list.
 - With the recipe still highlighted, click on Multi Analysis. This instructs the instrument not to scan the sample again but to reanalyze the data according to the recipe's data analysis parameters. (Note that the Multi Analysis button is not active (grayed out) for the first recipe in a sequence.)
 - Repeat the process as many times as needed.
5. Click on Start to scan the sample. A Save dialog box appears. Type in a name to save the multiple analysis recipe and to start the scan.

When the scan is complete, the scan trace for the first recipe (Site 1) appears on the screen.

To view results:

1. Tile the windows to display the Sequence Parameter Summary window and the Scan Trace simultaneously.
2. Click in the Sequence Parameter Summary window to activate it. Site 1 shows data analyzed with the first recipe in the sequence list; Site 2 data corresponds to the second recipe, and so on.
3. To view each recipe's data set in both Trace and Summary windows, click first on the arrow in the Recipe drop down box in the menu bar and then click on the recipe's name. You can also click on the Site box in the summary table.
4. To teach cursor positions (possible only if the recipe is new), display the trace for the desired recipe and set the level and measurement cursors as desired. Select Recalc from the Operations menu to enter the new cursors in the recipe.
5. Save the data set as desired.

8.6 VIEWING WAFER SUMMARY DATA

The Sequence Parameter Data window displays the results of a sequence based on an individual wafer within a cassette, as well as across a sequence of wafers for the entire cassette. This information includes detailed data about one or more sites scanned on a single wafer.

To display the wafer summary data:

Select Sequence Parameter Data from the Window menu of the Data Analysis window, as shown in Figure 8-11.

Tencor Instruments					
Analysis - [Sequence Parameter Data]					
File Trace Operations Window Help					
JFSREC1					
Lot: JFSSEQ1 Sequence: JFSSEQ1					
Op: Recipe: JFSREC1					
Deskew	Sample	Stat	Analyze	Height	TIR
	Cassette	Mean		-1.43692 μm	1.40128 μm
		S. D.		134.4 \AA	111.0 \AA
		Min		-1.46493 μm	1.38776 μm
		Max		-1.42182 μm	1.42381 μm
		Range		431.1 \AA	360.5 \AA
Passed	Slot 3	Mean	Inc	-1.43692 μm	1.40128 μm
		S. D.		134.4 \AA	111.0 \AA
		Min		-1.46493 μm	1.38776 μm
		Max		-1.42182 μm	1.42381 μm
		Range		431.1 \AA	360.5 \AA
Failed	Slot 5		Exc (Dskw)		
Passed	Slot 3				
	Site 1		Inc	-1.43050 μm	1.39625 μm
	Site 2		Inc	-1.42348 μm	1.39106 μm
	Site 3		Inc	-1.42964 μm	1.39427 μm
	Site 4		Inc	-1.42182 μm	1.38776 μm
	Site 5		Inc	-1.43318 μm	1.39948 μm
	Site 6		Inc	-1.44752 μm	1.41086 μm
	Site 7		Inc	-1.46493 μm	1.42381 μm
	Site 8		Inc	-1.43909 μm	1.40216 μm
Substr.					

Figure 8-11 Sequence Parameter Data Window

To view the entire Sequence Parameter Data screen from the Trace window, you need to maximize the Sequence Parameter Data window.

Using the Sequence Parameter Data window, you can select recipes from the pull-down list on the left of the tool bar. This pull-down list displays all recipes that are included in the sequence.

To specify data on the Sequence Parameter Data window:

Select Sequence Summary Options from the Operations menu of the Data Analysis window, as shown in Figure 8-12 below.

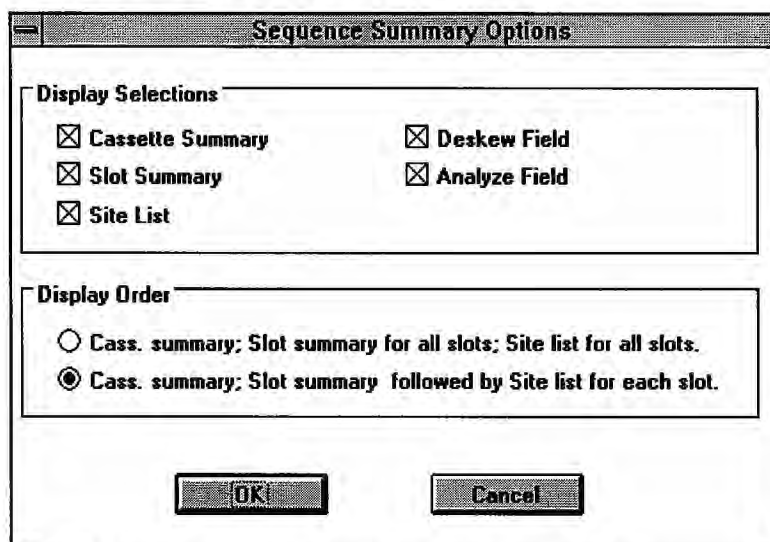


Figure 8-12 Sequence Summary Options Window

The Sequence Summary Options window lets you specify the information on the Sequence Parameter Data window, including data for each site scanned on a slot (wafer) for the entire cassette or for an individual wafer within a cassette.

You can view the Trace window for any of the sequence steps by clicking on the appropriate site number in the Sequence Parameter Data window.

To view Sequence data with the corresponding trace, site-by-site:

You can easily set up the screen to display a site's parameter data along with the trace itself.

1. Open both Trace And Sequence Parameter Data windows.
2. Choose Tile Vertically from the Windows menu.
3. Size the windows to your satisfaction by clicking and dragging their frames.
4. In the Sequence Parameter Data window, click on the numbered Site box of the trace desired. The Trace window displays the trace for that site. Repeat for other sites, displaying each trace in turn.
5. To preserve this window orientation, select Save Workspace from the File menu. In the dialog box that appears, give the workspace a filename and click OK to save it.

The next time you want to review both parameter data and trace, retrieve the workspace by choosing Load Workspace from the File menu. Then highlight the workspace name in the drop-down menu and click OK. The screen reconfigures to the identical trace/data window orientation.

8.7 TEACHING THE BASE ANGLE

The Base Angle is an offset angle relative to a wafer's flat or notch. It is used to align scans with the wafer geometry. The Base Angle is fixed for all scans in the sequence. You can program this offset in the Teach Location window.

To teach the Base Angle:

1. Double-click on the Base Angle step in the sequence list. The Teach Location window appears (Fig. 8-9).
2. Locate a line or die grid pattern to use for a reference.
3. Click on the clockwise or counterclockwise rotation buttons in the tool bar until the cross hairs are aligned with the reference feature. You might have to move the stage to keep the reference feature in the field of view as you rotate.
4. Click on OK, or press ENTER, to return to the Sequence Editor window. Note that the Base Angle now has a value instead of the phrase "not used."

When you run a sequence with a non-zero Base Angle, the stage will rotate to that position immediately after the Video Calibration step (if used) and before taking scans.

8.8 SEQUENCING WITH MANUAL DESKEW

The reason for programming a sequence is to speed up a repetitive series of measurements on one or more samples. The example in Section 8.4, "A Simple Sequence Example," contains all of the essential features of a sequence.

However, its usefulness is limited by the fact that no specific reference points were established. This might not be a problem if a precision locator is being used to position each sample on the stage and if the features being measured are relatively large.

Without a locator or some sort of fixture, or without using the wafer handler, you would run into problems reusing this first sequence to measure another of these samples. Without fixturing, you cannot reliably put the second and subsequent samples on the stage in the same position and with the same alignment as the first. You can still use the sequence you have written, but you would have to manually find each of the scan sites and reteach them before running the sequence.

Deskew enables you to identify two points on a sample to use as reference points prior to the start of a sequence. These points are then used to correct mathematically for translational (X, Y) and rotational (theta) error in sample positioning.

Note, however, that though a coordinate transformation is made, there is no stage rotation to compensate for the small rotational error in sample placement unless you set the deskew options to perform a second deskew. See Section 8.9, "Deskewing Twice to Align Theta," for more information.

Note also that any rotational error will be magnified when you traverse a long distance across a large wafer. This might cause the deskew site to be outside the field of view when a wafer is loaded.

NOTE: To minimize positioning error, space the deskew points approximately one-half the diameter of the sample. Do not set the deskew points parallel to the X- or Y-axis, but instead use two points on a diagonal line. If the deskew points are identical, the sequence aborts.

When programming sites, choose a logical progression to reduce the total distance traveled and to save time, as in the following figure.

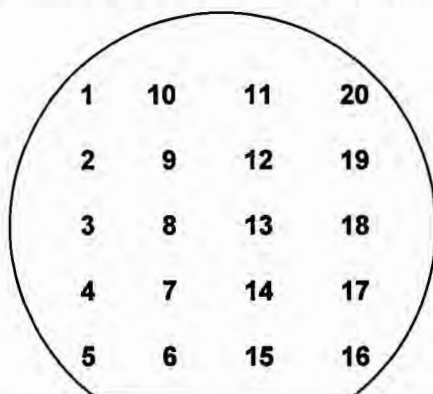


Figure 8-13 Logical Order of Sequence Sites

To set up a sequence with Manual Deskew:

1. Bring up the Sequence Editor window by choosing View/Modify from the Sequence menu of the Scan Application window.
2. To make sure you begin with a blank sequence, choose New from the Sequence menu. Two entries, Video Calibration and Base Angle, appear in the sequence list on the right side of the window. The mode is set as No Deskew and the Data and Handler options are set to their defaults. (A Video Calibration step appears at the beginning of every sequence to assure accurate results for scan length teaching and for Pattern Rec. Base Angle is an offset angle relative to the wafer's flat or notch.)
3. Set the Deskew mode to Manual Deskew. Note that two deskew steps now appear in the sequence list on the right side of the window.
4. Select the first deskew site by clicking anywhere on the Deskew Site 1 line in the sequence list, or use [^] and [v] to move the selection bar to Deskew Site 1.
5. Click on the Teach control button, or double-click on the selected sequence step. The Manual Deskew Teach window appears (Fig. 8-14).

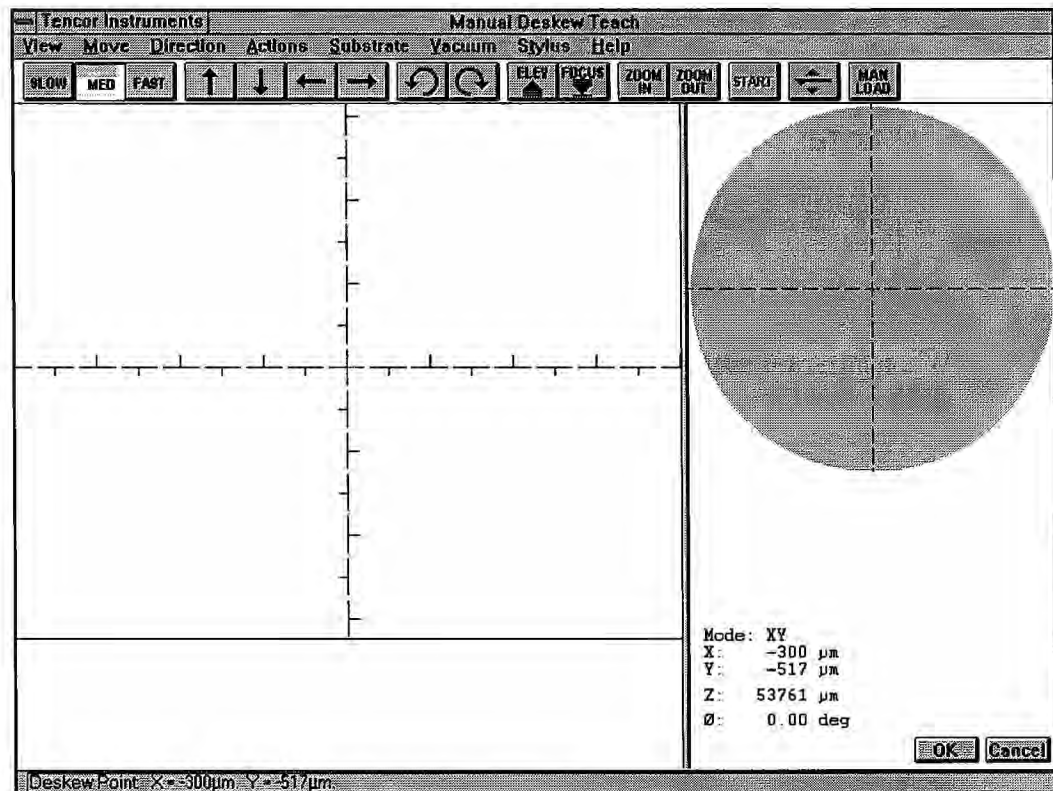


Figure 8-14 Manual Deskew Teach Window

6. Choose a site for the first deskew point. Choose an obvious point, such as the corner of an easily identifiable rectangle. Click on the chosen position. The stage will move so that the cross hairs are centered on the selected site.
7. Click on OK. The Sequence Editor window reappears, with the X and Y coordinates of the selected site entered in the Deskew Site 1 step.
8. Select Deskew Site 2 and repeat steps 5–7 for the second deskew site.
9. Once the deskew sites have been successfully established, proceed to programming the rest of the sequence steps.
10. Run the sequence. After each deskew operation, the instrument pauses and waits for you to accept the deskew sites by clicking on OK.

8.9 DESKEWING TWICE TO ALIGN THETA

With a single deskew operation, there is no stage rotation to compensate for the small rotational error in sample placement. You can choose to perform a second deskew to compensate for this error by enabling this option in the Deskew Options dialog box. This allows accurate sample rotations within a sequence.

To set deskew options to perform a second deskew to align theta:

1. From the main Configuration window, click on the Deskew Options button. The Deskew Options dialog box appears:

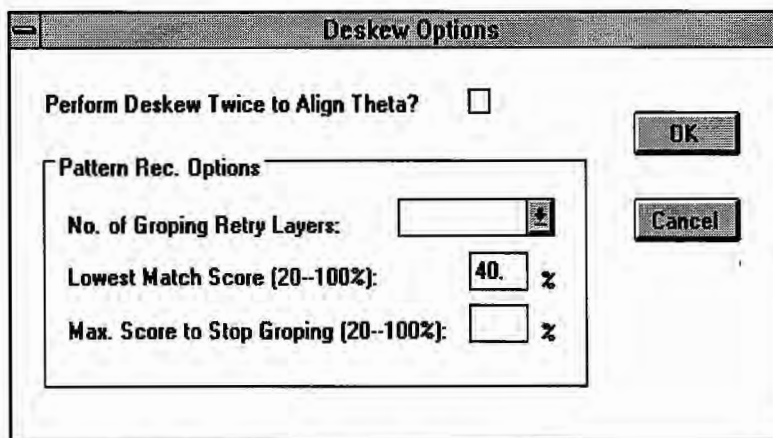


Figure 8-15 Deskew Options Dialog Box

2. Click on the check box to enable or disable the second deskew.
3. When finished, click on OK to set the options and close the dialog box, or Cancel to close the dialog box without changing the previous settings.

8.10 SEQUENCING WITH PATTERN RECOGNITION DESKEW (PATTERN RECOGNITION OPTION ONLY)

The Pattern Recognition option allows greater throughput in sequence operation by automating the precise setting of deskew points at the beginning of a sequence.

A pattern recognition deskew site is a unique pattern of wafer features visible within the instrument's field of view. The size and shape of the pattern must be uniquely different from other wafer features visible in the field of view to ensure that the instrument can locate the sites without ambiguity.

Some examples of good patterns are

- Alphanumeric characters
- Circular or rectangular pads that appear singly
- Crosses
- Alignment marks
- Other polygon shapes

Some examples of bad patterns are

- Sections of a repetitive grid
- Circular pads or rectangular pads that repeat in or near the field of view

When choosing patterns, keep the following points in mind:

- *Search time depends on pattern size.* The larger the pattern, the faster the instrument computer can recognize the pattern. Note: Larger patterns require more accurate initial positioning within the camera's field of view because the search area is reduced.

Also, you can set the Pattern Recognition options so that the system will perform a pattern search if the pattern is not found within the field of view. See Section 8.11, "Pattern Recognition Deskew Options," for information.

- *When using rectangular pads, use the entire rectangle.* If only two corners are used, other rectangles in the field of view could confuse the pattern recognition system.
- *The pattern should be unique and as simple as possible.* However, uniqueness cannot be sacrificed for simplicity.
- *Choose symmetric patterns.* They are less sensitive to image rotation. Circular patterns are rotationally symmetric and therefore are good patterns. Similarly, the best polygon patterns have the most sides.
- *High contrast features make pattern recognition matches easier.* When available, choose high contrast features. Noise will not have as much effect on the pattern recognition match. The pattern colors are important because the pattern recognition system reads the black and white image, not the color image. A pattern with good color contrast might not have good black and white contrast. For example, avoid yellow-on-white or white-on-yellow patterns, since these color combinations have almost zero black and white contrast.
- *Avoid patterns with rough surfaces.* By using edge enhancement, the instrument computer emphasizes the fine features present on a rough surface. Because roughness is random, these features add noise to the system and make the pattern recognition system less reliable.

It is generally a good idea to avoid fixed dust particles in the field of view as well. Avoid selecting wafer-specific defects or features as patterns, or you might confuse the instrument computer. This includes dust particles, partially etched areas near the edge of the wafer, and so on.

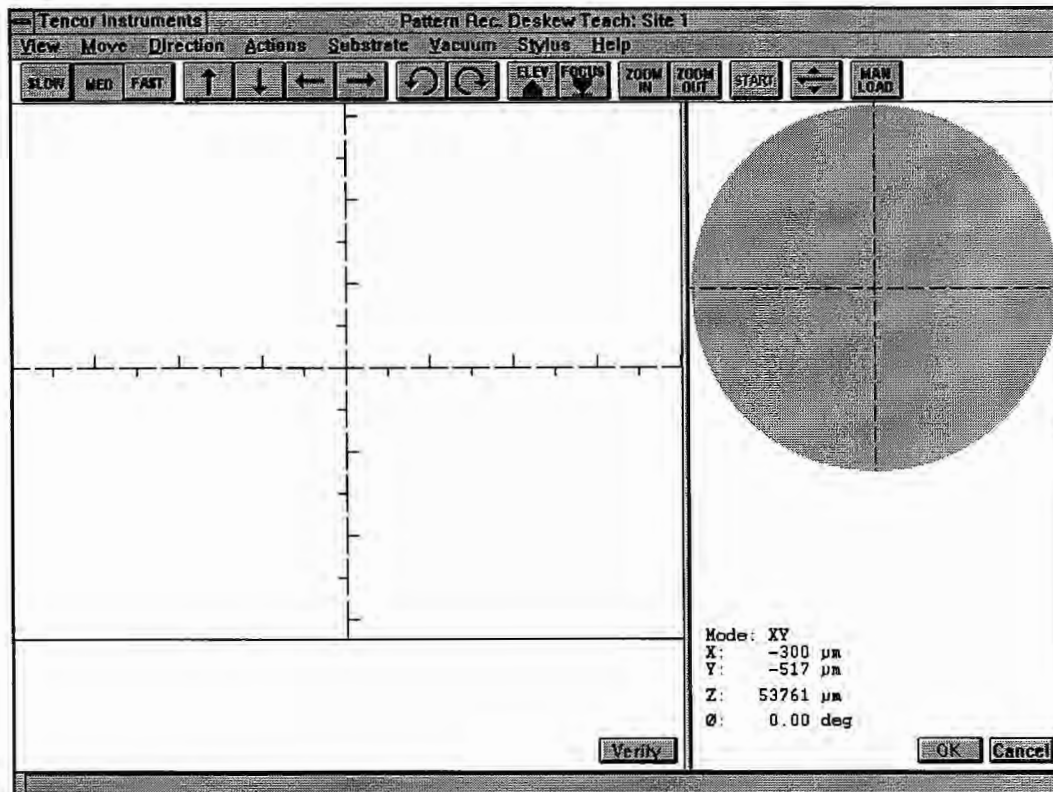
Semi-Automatic mode allows you to manually adjust the position of the stage in case the deskew site does not appear in the field of view when the sequence begins.

Due to the number of variables that affect pattern recognition, the computer may not always be successful in locating a deskew site. You can preset the instrument to do one of four things in the event of a failure:

- continue scanning;
- stop scanning the wafer and proceed to the next;
- repeat the pattern recognition; or
- stop the entire sequence and wait for operator intervention.

To set up a sequence with Pattern Rec. Deskew:

1. In the Sequence Editor window, select Pattern Rec. Deskew from the Mode drop-down box.
2. Double-click on the DESKEW1 entry near the top of the sequence list or highlight the DESKEW1 entry and click on Teach. The Pattern Rec. Deskew Teach window appears and the stylus automatically nulls on the sample surface.

**Figure 8-16 Pattern Rec. Deskew Teach Window**

3. Choose a pattern to use for pattern recognition. As a rule of thumb, select something that is simple and easily recognizable, like an alphanumeric character or an alignment mark. Something that looks much like another feature that is also within the field of view does not work reliably because the wrong site might be identified.
4. Define a rectangular area that encloses the chosen pattern as follows:
 - Press the left trackball button at one corner of the desired rectangle.
 - Move the trackball toward the opposite corner of the desired rectangle. A blue box appears that follows the trackball cursor as it moves.
 - When satisfied with the desired rectangular area, release the trackball button.

The instrument computer processes the image information defined by the rectangle. If the rectangle was too small, a message box appears. Click on the OK button and reteach the pattern.

- The blue box remains on the window with a darker blue dot in the center. The stage moves until the selected feature is centered in the cross hairs (Fig. 8-17).

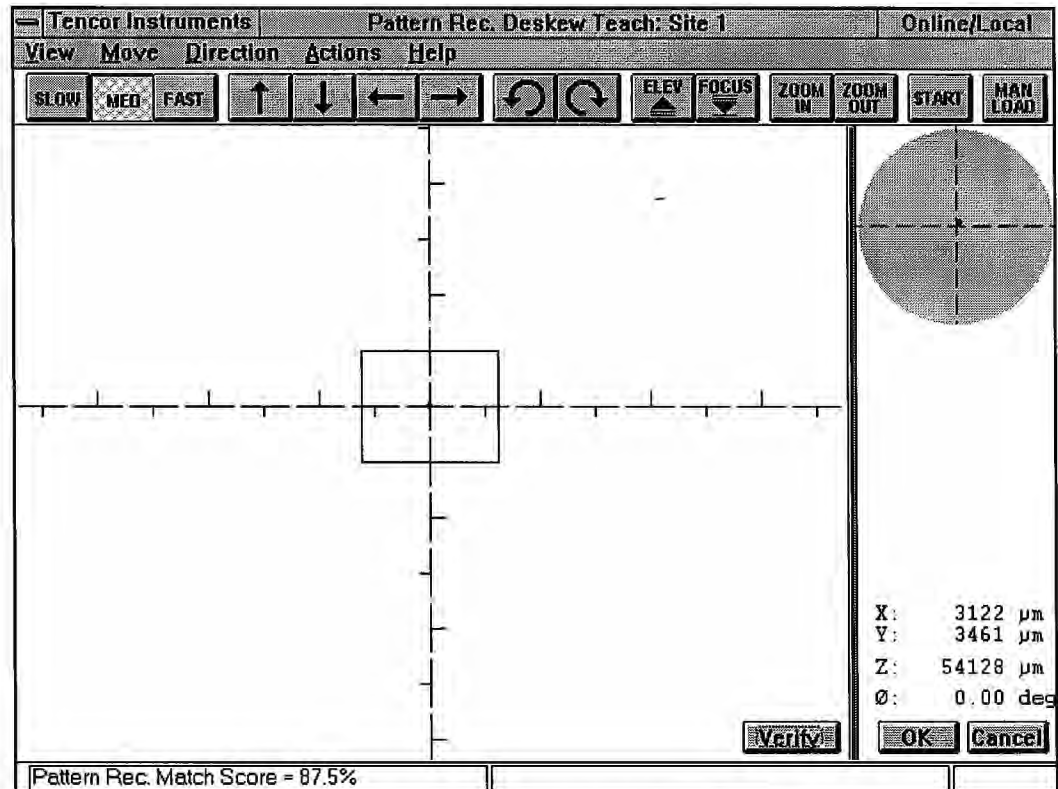


Figure 8-17 Pattern Rec. Deskew Teach Window After Teach

- Move the stage a small distance, then click Verify to test whether the system can accurately find the feature you have taught. A box is drawn around the feature when it is found. If recognition fails, repeat Step 3 and retry.
- Click on OK to accept the taught pattern, or click on Cancel to quit the Teach Pattern Rec. Deskew window without saving the taught pattern.
- Repeat for the DESKEW2 step to establish the second deskew point.
- Once the deskew sites have been successfully established, proceed to programming the rest of the sequence steps.
- Run the sequence.

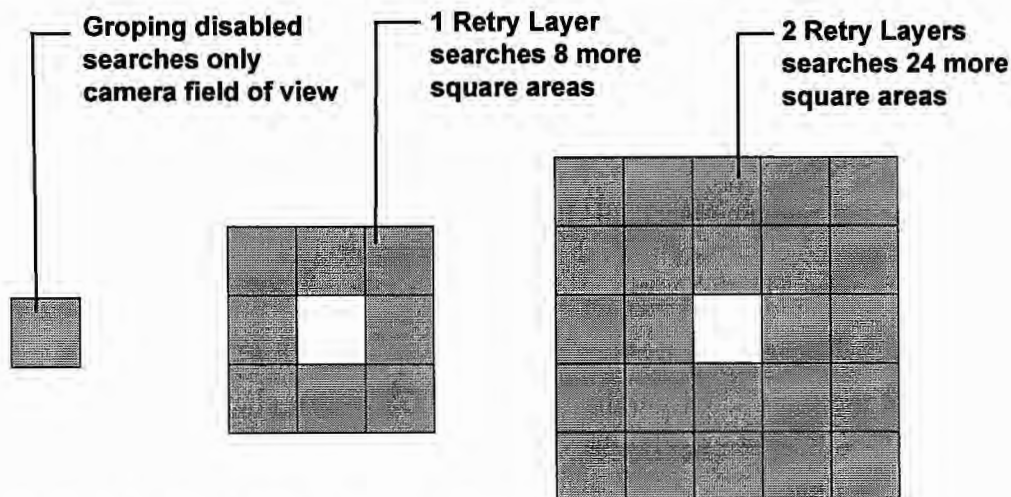
8.11 PATTERN RECOGNITION DESKEW OPTIONS

You can set Pattern Recognition options so that the system performs a pattern search if the pattern is not found within the field of view when the sample is positioned at the deskew site. This search is called *groping*.

The three groping parameters are described below.

NUMBER OF GROPING RETRY LAYERS

This parameter controls how much of the area around the deskew site is searched for the pattern. Each layer consists of a square area constructed by evenly surrounding the deskew site with squares the size of the camera field of view (Fig. 8-15):



Similarly for 3 and 4 Retry Layers (48 and 80 square areas)

Figure 8-18 Groping Retry Layers

Available choices are

- Disabled (the default)
- 1 (8 Sites)
- 2 (24 Sites)
- 3 (48 Sites)
- 4 (80 Sites)

First, the deskew site field of view is searched. If the pattern is not found, the stage moves to one corner of the next layer and searches the field of view there. This continues until the pattern is found or until all search sites have been examined. If the pattern is still not found, the stage moves to one corner of the next layer and continues.

Note that if it takes 10 s to move the stage, null the stylus, and search one such area, 8 search sites (1 layer of retry) takes as long as 90 s, 24 sites (2 layers) takes as long as 250 s, and so on.

LOWEST MATCH SCORE

This parameter allows you to adjust the threshold at which the pattern recognition system will conclude that it has found a candidate for the desired deskew site. If the pattern does not show up in the original field of view, the search begins, and if any matches score greater than the Lowest Match Score, the pattern recognition system concludes that the best of

these is the correct site for the deskew site (unless it finds a match equal to or greater than the Maximum Score to Stop Groping). Allowed values range between 20–100%.

MAXIMUM SCORE TO STOP GROPING

If the pattern recognition system is groping to find the desired pattern, sometimes the matching pattern is found with little ambiguity. Usually a large number such as 90% means that the pattern has been found. In this case, there is no reason to continue searching the retry layer. If a score equal to or better than the Maximum Score to Stop Groping occurs, the searching process stops and the deskew site is placed.

Allowed values range between 20–100%. If no matches are found that are as good as this setting, the search continues until the retry layer areas are all searched, and the best score above the Lowest Match Score setting determines the placement of the deskew site.

To set Pattern Recognition deskew options:

1. From the main Configuration window (Fig. 5-26), click on the Deskew Options button. The Deskew Options dialog box appears (Fig. 8-15).
2. Edit the fields.
3. When finished, click on OK to set the options and close the dialog box, or Cancel to close the dialog box without changing the previous settings.

8.12 SEQUENCING WITH THE WAFER HANDLER

This section discusses sequences using the wafer handler with sequences. The wafer handler makes it possible to measure a sequence on as many as 26 individual wafers without operator intervention.

The wafer handler can be configured to load wafers of four different sizes:

- 100 mm (4 in.)
- 125 mm (5 in.)
- 150 mm (6 in.)
- 200 mm (8 in.)

The standard system configuration includes one cassette locator for 200-mm wafers. A second locator is available as an option. For 100-, 125-, or 150-mm wafers, an additional locator plate for each size attaches by thumbscrew on top of the 200-mm locator.

For satisfactory operation, the handler chuck must be installed (see “Installing a Precision Locator” in the *Tencor P-20h Long Scan Profiler Reference Manual*) and the elevator limit properly set (see Section 5.8.4, “Lowest Elevator Position”).

Before operating the wafer handler for the first time, read Section 2.7.1, "Protecting the Wafer Handler," for important information on protecting the wafer handler and wafer from damage.

NOTE: Cassettes should be the same size and type that Tencor Instruments Field Service taught the wafer handler. Cassettes that have been used in chemical processing, which causes distortion, can make it difficult for the handler to center the wafers on the vacuum puck and stage. Dedicated machine cassettes are best.

Before using the handler, check the following:

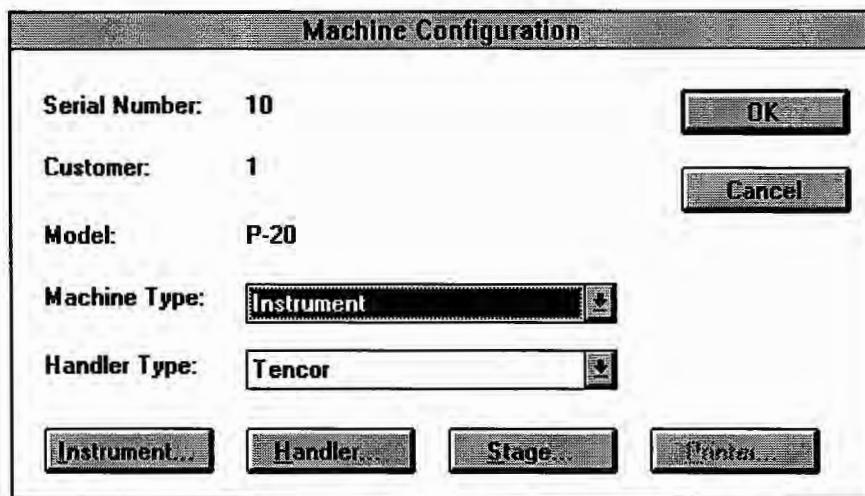
- The vacuum chuck is installed on the stage table.
- The handler parameters are set up properly.
- The wafer size is properly set for the aligner.

The instrument is shipped with the vacuum chuck installed..

CAUTION: Do not use a precision locator when using the handler to load wafers; you could damage the instrument.

To set handler parameters:

1. From the Top Level menu, double-click on Configuration. From the main Configuration window, click on System Configuration. The Machine Configuration dialog box appears:

The image shows a 'Machine Configuration' dialog box. It has a title bar with the text 'Machine Configuration'. Inside the dialog, there are several fields: 'Serial Number:' with the value '10', 'Customer:' with the value '1', 'Model:' with the value 'P-20', 'Machine Type:' with a dropdown menu showing 'Instrument', and 'Handler Type:' with a dropdown menu showing 'Tencor'. To the right of these fields are 'OK' and 'Cancel' buttons. At the bottom of the dialog, there are four buttons: 'Instrument...', 'Handler...', 'Stage...', and 'Print...'.

Serial Number:	10	OK
Customer:	1	Cancel
Model:	P-20	
Machine Type:	Instrument	
Handler Type:	Tencor	
Instrument...		Handler...
Stage...		Print...

Figure 8-19 Machine Configuration Dialog Box

- Click on the Handler button. The Handler Setup dialog box appears.

General Information	
Handler Type:	Tencor
Wafer ID Type:	None
Number of Slots:	25

Cassette Information	
Place	Cassette Name
<input checked="" type="checkbox"/> Cassette #1	RECEIVER
<input checked="" type="checkbox"/> Cassette #2	SENDER

Figure 8-20 Handler Setup Dialog Box

- Edit values as needed. When finished, click on OK to keep the changes, or Cancel to close the dialog box and leave the setup in its original state.

Handler parameters are set up in the Configuration window. Values for the handler parameters are set as follows:

Handler Type

Handler Type can be either Tencor or None.

Wafer ID Type

Wafer ID Type can either be None or OCR.

Number of Wafers

This field identifies the capacity of the wafer cassettes used. The possible choices are 25 or 26.

Cassette Information

These fields specify the number of cassettes used by the handler and how they are used. An X in the check box for a cassette indicates that the particular cassette is present on the instrument. The Cassette Name fields identify the particular cassette is either the Sender, Receiver, or Both. (If only one cassette is available, it must serve as both the receiver and the handler.)

To set the wafer size on the aligner:

Turn the wafer size selector dial on the aligner (Fig. 8-21) until it displays the appropriate wafer diameter.

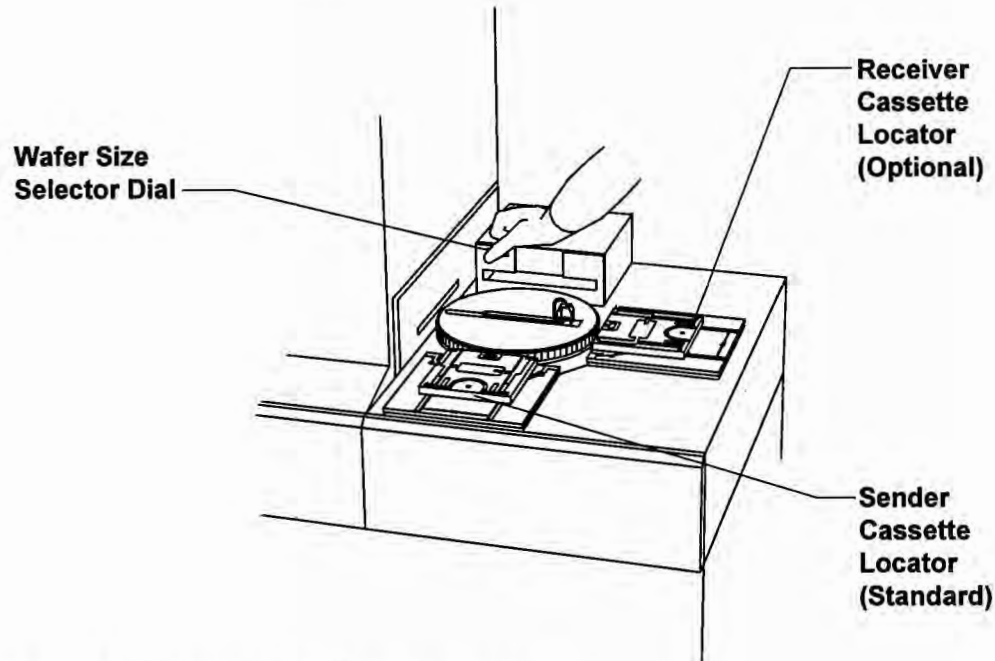


Figure 8-21 Setting the Wafer Size Selector

To prepare for loading wafers using the handler:

1. Place the wafers in the slots of a cassette of the appropriate size. Load the wafer right side up. The bottom slot of the cassette is number 1.
2. Place the cassette on the sender cassette locator (Fig. 8-22) as follows:
 - Tilt the cassette back slightly and place the bottom rear corners of the cassette in the grooves on the locator. The grooves are marked with wafer sizes (100 mm, 125 mm, 150 mm, and 200 mm).
 - Tilt the cassette forward until it fits securely in the grooves of the cassette locator. The H-bar across the bottom of the cassette must trip the limit switch in the slot on the locator.

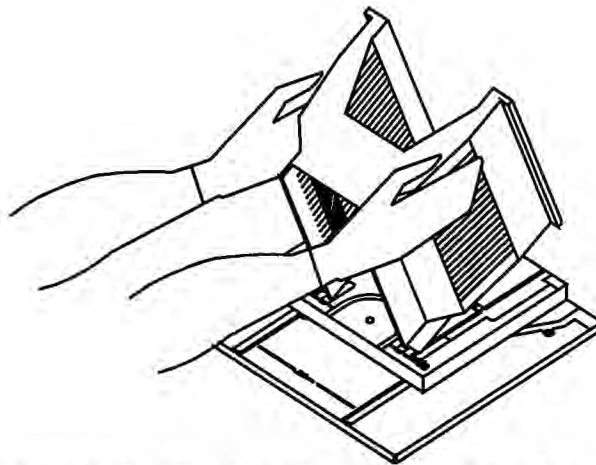


Figure 8-22 Placing a Cassette on a Locator

3. If you have two cassette locators, you can use the second one to receive wafers.

NOTE: Cassettes placed on both locators must be the same size. Otherwise, wafers could be damaged and handler performance could be affected. Reinitialize the handler each time the cassette size is changed.

4. In the Sequence Editor, click on Handler Options. The following dialog box appears:

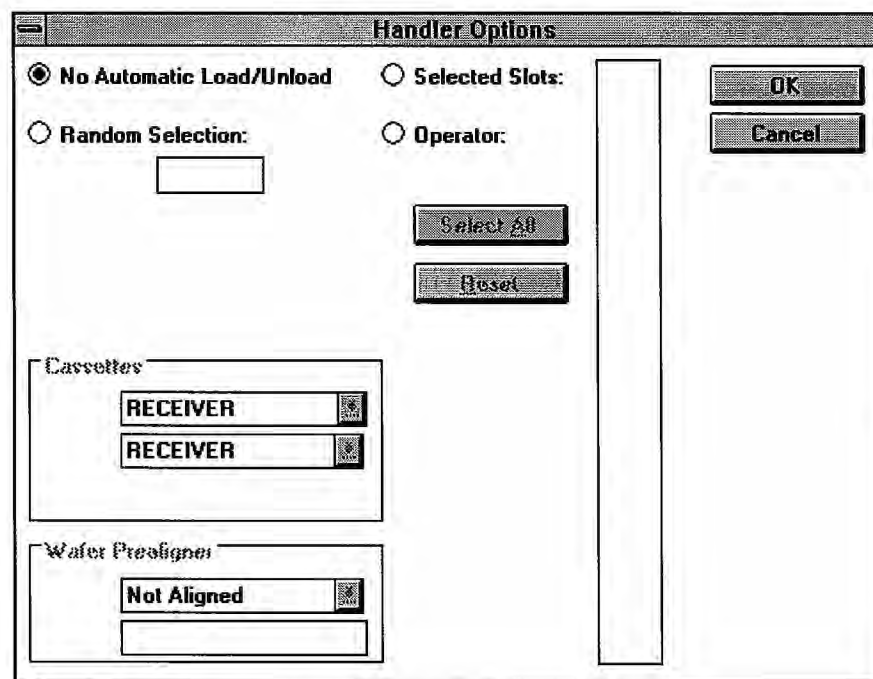


Figure 8-23 Handler Options Dialog Box

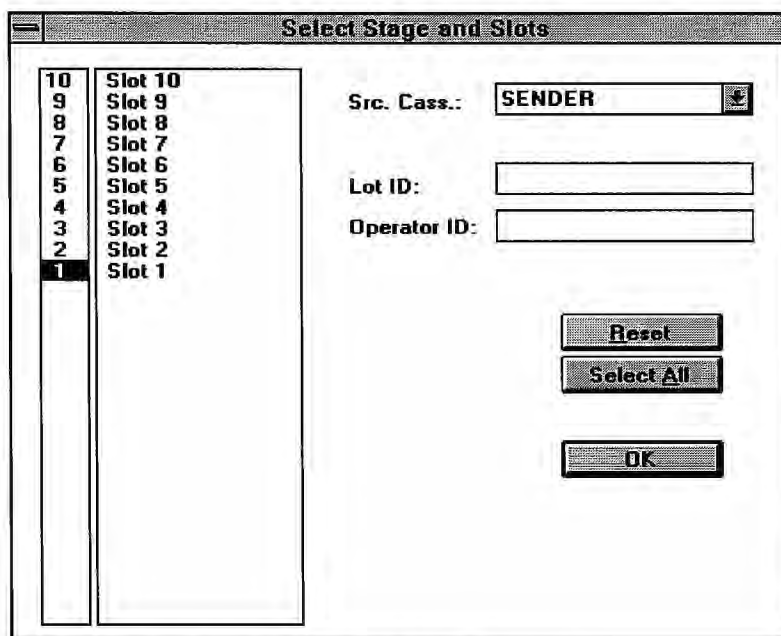
The Handler Options include wafer selection settings, cassette selection, and wafer prealignment settings. When finished choosing options in this window, click on OK to set the options and close the dialog box, or Cancel to close the dialog box without changing the previous settings.

The Handler options are described as follows.

Wafer Selection Settings

To select a setting for wafer selection, click on the appropriate radio button. The available choices are

No Automatic Load/Unload	The sequence does not automatically load and unload wafers; loading and unloading are performed manually.
Random Selection	A specified number of wafers are randomly selected from the cassette. The desired number (1–25 or 1–26) is typed into the text box just below the Random Selection radio button. Wafers are loaded and unloaded without operator intervention. This can only be selected with a full cassette of wafers.
Selected Slots	<p>A specified number of wafers, in specific cassette slots, are loaded and unloaded.</p> <p>To select or unselect specific wafers, click on the numbers in the tall list box to the right of the Selected Slots radio button. You can also click on the Select All button to select all 25 wafers, or click on the Reset button to clear all selections.</p>
Operator	<p>Similar to Selected except that at the start of the sequence, the Handler Options dialog box appears to allow the operator to modify the original slot selection before the sequence commences.</p> <p>Additionally, the Operator mode allows you to enter Slot ID, Lot ID, and Operator ID. Fig. 8-24 shows a 10-slot cassette.</p>

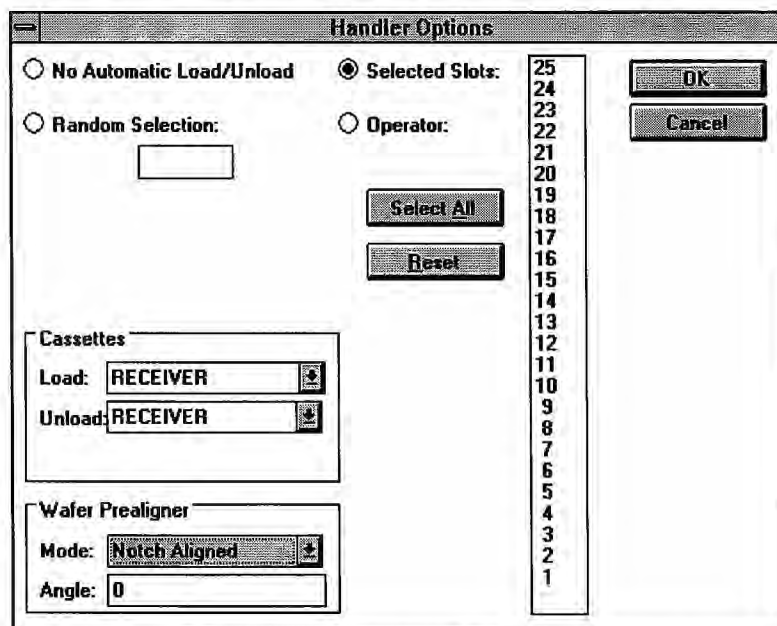


The "Select Stage and Slots" dialog box features a list of slots on the left, numbered 1 to 10, with "Slot 1" selected. To the right, there are input fields for "Src. Cass.:" (set to "SENDER"), "Lot ID:", and "Operator ID:". At the bottom right, there are three buttons: "Reset", "Select All", and "OK".

Figure 8-24 Select Stage and Slots Screen

Slot # is the slot identification that the user enters, Lot ID is the cassette name, and the Operator ID is any valid user name. This information appears on the Analysis report and printouts.

If Random Selection, Selected Slots, or Operator is chosen, the Handler Options window takes on a slightly different appearance (Fig. 8-25).



The "Handler Options" dialog box shows several configuration options. On the left, there are radio buttons for "No Automatic Load/Unload" (selected), "Random Selection:", and "Operator:". Below these are fields for "Cassettes" (Load: RECEIVER, Unload: RECEIVER) and "Wafer Prealigner" (Mode: Notch Aligned, Angle: 0). In the center, there are "Select All" and "Reset" buttons. On the right, there is a vertical list of slots numbered 1 to 25, with "Selected Slots:" at the top. At the bottom right, there are "OK" and "Cancel" buttons.

Figure 8-25 Handler Options Dialog Box with Slot Selection Enabled

When finished, click on OK to set the options and close the dialog box, or Cancel to close the dialog box without changing the previous settings.

Cassettes

The Cassettes section allows you to select which cassettes to use for loading and unloading wafers. The Load and Unload fields have the following possible settings:

Sender	Designates the Sender cassette as the wafer source or destination.
Receiver	Designates the Receiver cassette as the wafer source or destination. Note: The Receiver cassette locator is optional. Instruments without a Receiver cassette locator use the Sender cassette locator for both source and destination.

Wafer Prealigner

The Wafer Prealigner section contains configuration settings for the handler to prealign the wafers before placing them on the handler chuck.

The Mode field has the following possible settings:

Flat	Orients the wafer by its major flat.
Notch	Orients the wafer by its alignment notch.
None	Turns Wafer Prealignment off. The handler bypasses the aligner when it loads wafers. Bypassing the aligner increases throughput but it can also reduce the accuracy of centering the wafer on the stage.

If the Wafer Prealigner Mode is set to Flat or Notch, the Angle field is active and can accept any angle from 0°–360°. The Angle field specifies the position, in degrees, of the flat or notch when it is placed on the puck. A value of 0 causes the wafer to be placed on the handler chuck with the flat or notch to the front of the instrument, that is, the 6 o'clock position. When a wafer is loaded into a cassette, the flat or notch is rotated 90° and is at the 9 o'clock position.

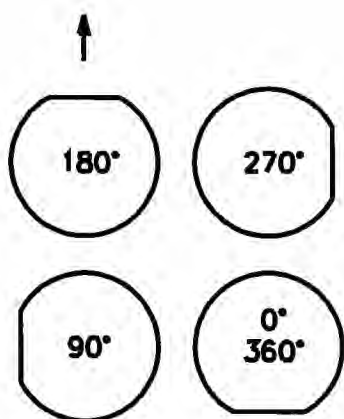


Figure 8-26 Wafer Orientation

8.13 SAVING AND MAINTAINING SEQUENCES

Once you have written a sequence that you want to keep for future use, you need to save it on the hard disk.

To save a previously saved sequence:

- Choose Save from the Sequence menu.
- Or click on the Save button in the tool bar.

To save a new sequence:

1. Choose Save As from the Sequence menu. The following dialog box appears:

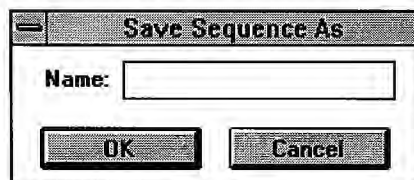


Figure 8-27 Save Sequence Dialog Box

2. Type a name for the sequence, then click on OK, or click on Cancel to abort the Save operation.

Sometimes you might want to edit an existing sequence, make a few minor changes, and save the result with a new name.

To save a sequence under a new name:

1. Choose Save As... from the Sequence menu. The Save Sequence As dialog box (Fig. 8-27) appears.

2. Type a name for the sequence. The sequence filename must be a valid DOS filename.
Valid DOS filenames
 - Can contain a maximum of eight characters
 - Have a three-character extension supplied by the system
 - Are not case-sensitive
 - Can contain only the letters A–Z, the numbers 0–9, and the following special characters: tilde (~), exclamation point (!), at sign (@), number sign (#), dollar sign (\$), percent sign (%), caret (^), ampersand (&), left parenthesis, right parenthesis, underscore (_), hyphen (-), left brace ({), right brace (}), single quotation mark ('), and apostrophe (')
 - Cannot be identical to the name of another existing sequence or scan recipe
3. Click on OK, or click on Cancel to abort the Save operation.

To load a sequence into the Sequence Editor:

1. In the Sequence Editor window, select Open from the Sequence menu. The following dialog box appears (Fig. 8-28):

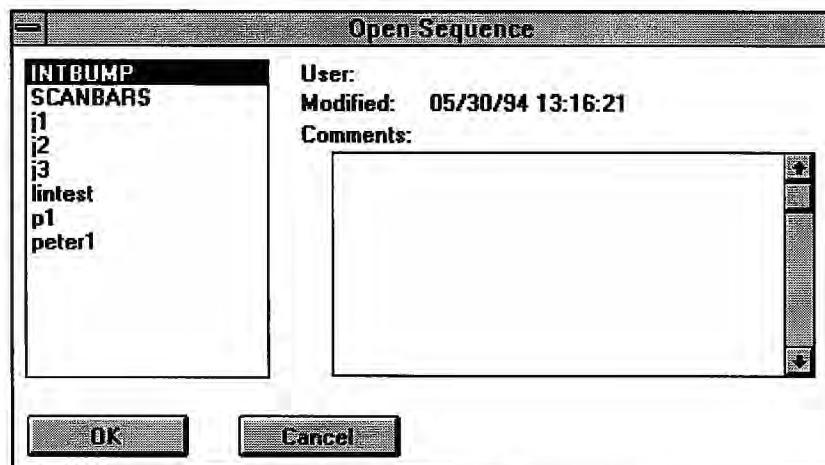


Figure 8-28 Open Sequence Dialog Box

2. Select the desired sequence from the list of sequences on the left side.
3. Click on the OK button.

8.14 SAVING AND MAINTAINING SEQUENCE SCAN DATA

Sequence scan data can be saved for reviewing at a later time.

To save sequence scan data:

1. Choose Save Data from the File menu. The following dialog box appears:

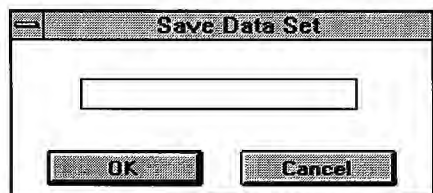


Figure 8-29 Save Data Set Dialog Box

2. Type a name for the data set, then click on OK, or click on Cancel to abort the Save operation. The data set filename must be a valid DOS filename. Valid DOS filenames
 - Can contain a maximum of eight characters
 - Have a three-character extension supplied by the system
 - Are not case-sensitive
 - Can contain only the letters A–Z, the numbers 0–9, and the following special characters: tilde (~), exclamation point (!), at sign (@), number sign (#), dollar sign (\$), percent sign (%), caret (^), ampersand (&), left parenthesis, right parenthesis, underscore (_), hyphen (-), left brace ({), right brace (}), single quotation mark ('), and apostrophe (')
 - Cannot be identical to the name of another existing data set

Once a data set has been saved, it is added to the Sequence Data catalog. The Sequence Data catalog window allows you to select individual data sets for reviewing. You can also delete unwanted data sets.

To view previously saved sequence data:

From the Catalog window, click on the Sequence Data button on the left side of the screen. The Sequence Data Catalog window appears:

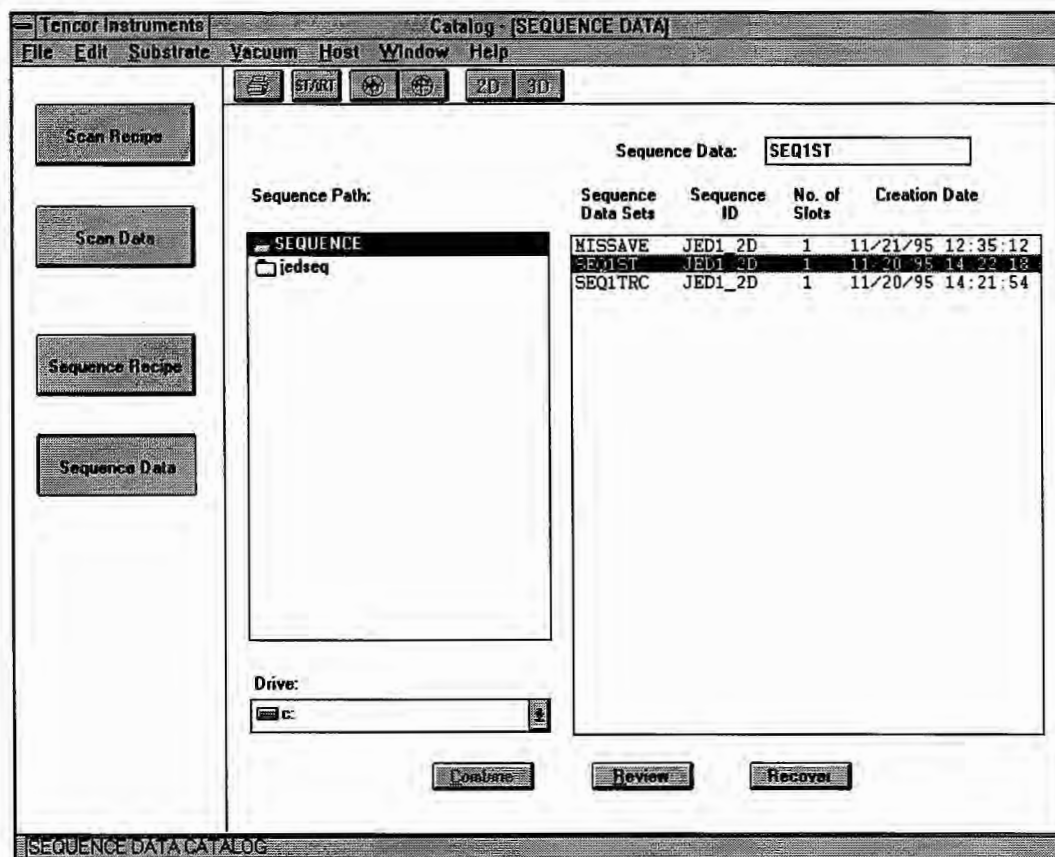


Figure 8-30 Sequence Data Catalog Window

To recover unsaved data:

You can recall to the screen the last data set displayed, including unsaved data, by clicking on Recover in the Sequence Data catalog window.

To review a data set:

Select the desired data set from the list in the catalog, and click on the Review button, or double-click on the desired data set.

To delete, import, and export sequences, see Chapter 9, "Using the Database."

8.15 COMBINED SEQUENCE STATISTICS (OPTIONAL)

You can calculate statistical data from multiple runs of a particular sequence. The computer accesses stored data from the data sets you select from the Sequence Data catalog and recalculates them. [Reviewers: is there a limit to the number of data sets? Is there other pertinent info about this feature?]

To obtain combined statistics:

1. From the Scan Recipe Catalog window, click on Sequence Data. The Sequence Data catalog appears.
2. Holding down CTRL, click on the data sets you would like included in the calculation. All must have the same Sequence ID. Those you have chosen will be highlighted.

A Save Data dialog box appears.

3. Type a name of the data set and click OK. A statistics summary with the new data appears after a short interval.

9 USING THE DATABASE

The Tencor P-20h database allows management of recipes and data. From the Database window, you can

- View the catalogs
- Delete files
- Print listings of files (recipe files only)
- Review recipes or data
- Export and import files (data files only)

9.1 DATABASE WINDOW

To open the Database window, click on the Export/Import icon on the Top Level menu (Fig. 3-2).

The main Database window appears with the Scan Recipe Catalog active. The Database window consists of the following elements:

- Menu bar
- Tool bar
- Secondary tool bar with a set of command buttons used to select which of the four database catalogs to display
- Main area of the window, displaying currently selected catalog and a series of command buttons

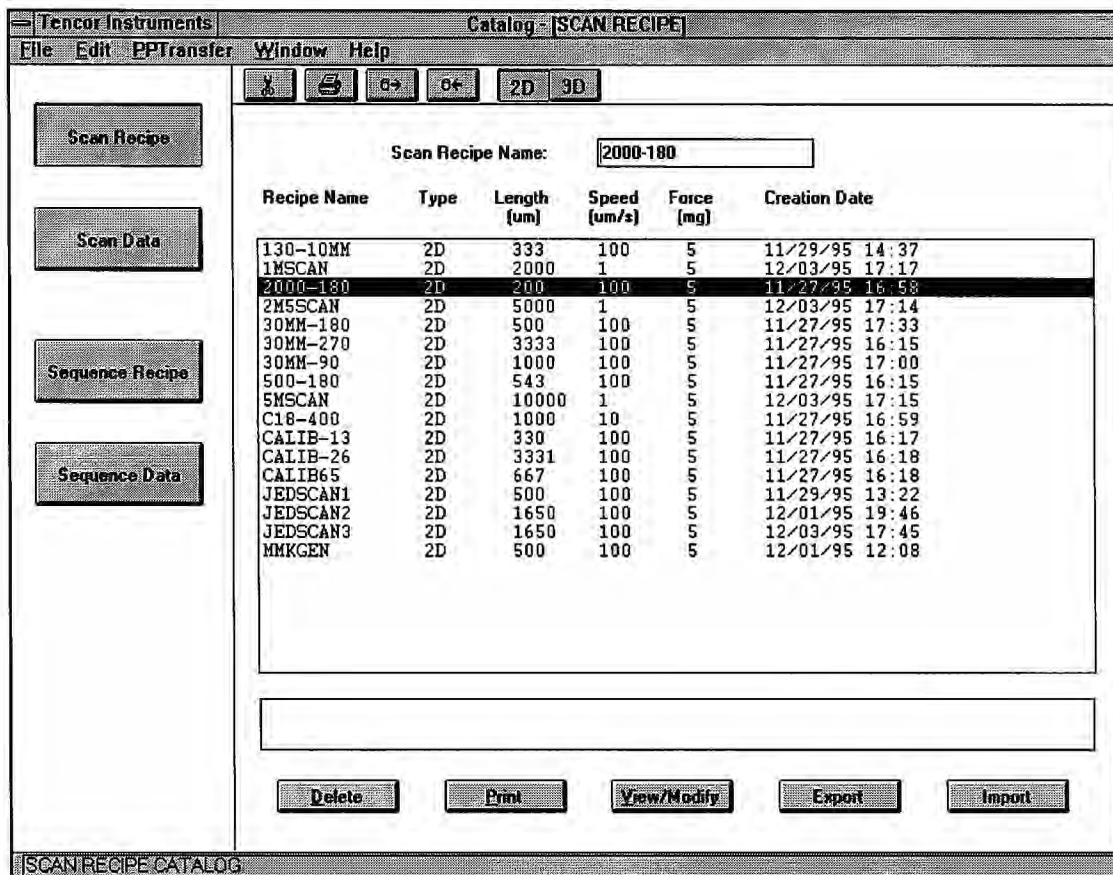


Figure 9-1 Database Window with Scan Recipe Catalog

9.1.1 DATABASE WINDOW MENU BAR

The Database window menu bar provides access to commands and allows easy navigating through the four subwindows.

The Database window menu bar provides the following menus. You can view menus by clicking on the titles in the menu bar, or by pressing ALT + *l*, where *l* is the letter that appears with an underscore in the desired title in the menu bar. You can choose menu items by clicking on a menu entry or by typing the letter that appears with an underscore in the desired menu item. Some menu items have hot keys assigned to them.



Figure 9-2 File Menu

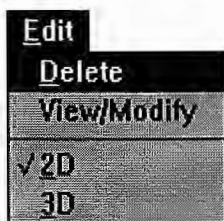


Figure 9-3 Edit Menu



Figure 9-4 PPTransfer Menu

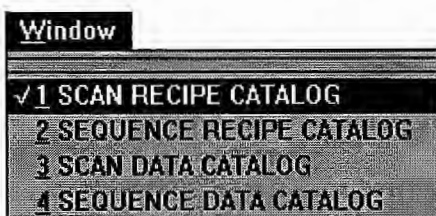





Figure 9-5 Window Menu




9.1.2 DATABASE WINDOW TOOL BAR

The Database window tool bar contains a row of icons that resemble buttons. Clicking on these icons provides an alternative way to access commonly used functions.

Each icon suggests the function of the button. For example, the Print button resembles a printer. Buttons that appear dimmed are unavailable.

The Database window tool bar contains the following buttons:





Button	Action
	Deletes the indicated recipe or data set
	Sends the indicated Scan or Sequence recipe to the printer
	Displays the Export dialog box

Button	Action
	Displays the Import dialog box
	Displays 2D scan data files
	Displays 3D scan data files

9.1.3 DATABASE WINDOW COMMAND BUTTONS

You choose which database catalog to maintain by selecting one of the four command buttons on the left side of the window. These buttons are visible at all times in the Database window and allow you to quickly change catalogs.

The following command buttons appear:

Button	Action
	Switches the main window to the Scan Recipe catalog
	Switches the main window to the Sequence Recipe catalog
	Switches the main window to the Scan Data catalog
	Switches the main window to the Sequence Data catalog

To select a group of parameters to view and edit:

Click on the appropriate command button, or select the appropriate catalog from the Window menu. The right side of the window displays the selected catalog.

9.2 DELETING DATABASE ITEMS

You can delete Scan and Sequence recipes and data from the appropriate catalog.

To delete a database item:

1. Display the desired catalog by clicking on the appropriate command button on the left side of the window.
2. Select the item you wish to delete by clicking or scrolling with the arrow keys.
3. Click on the Delete button below the catalog, or the Delete icon in the tool bar. The following dialog box appears.

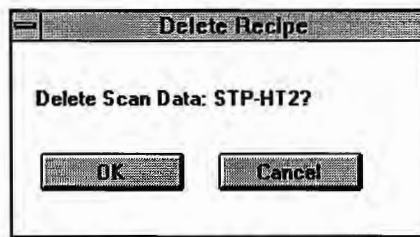


Figure 9-6 Delete Recipe Dialog Box

4. Click on OK to delete, or Cancel to leave the selected item in the catalog.

9.3 PRINTING DATABASE ITEMS

You can print a listing of Scan or Sequence recipes from the appropriate catalog.

To print a Scan or Sequence recipe to the currently active printer:

1. Display the Scan Recipe or Sequence Recipe catalog by clicking on the appropriate command button on the left side of the window.
2. Select the recipe you wish to print by clicking or scrolling with the arrow keys.
3. Click on the Print button below the catalog, or the Print button in the tool bar.

To print a Scan or Sequence recipe to a selected printer:

1. Display the Scan Recipe or Sequence Recipe catalog by clicking on the appropriate command button on the left side of the window.
2. Select the recipe you wish to print by clicking or scrolling with the arrow keys.
3. Select Print from the File menu. The Print dialog box appears.
4. Select the desired printer from the list box and click on OK.

For more information on printing, see "Setting Up Printers" in the *Tencor P-20h Reference Manual*.

9.4 REVIEWING DATABASE ITEMS

You can select an item in any of the available catalogs to review. This opens the appropriate window with the selected item displayed.

To review a database item:

1. Display the desired catalog by clicking on the appropriate command button on the left side of the window.
2. Select the item you wish to delete by clicking or scrolling with the arrow keys.
3. Click on the Review button below the catalog. The appropriate window appears with the selected item displayed:
 - From the Scan Recipe catalog: the Recipe Editor

- From the Sequence Recipe catalog: the Sequence Editor
- From the Scan Data catalog: the Data Analysis window
- From the Sequence Data catalog: the Sequence Data window

From the Editor windows, you can edit recipes and save the changes before returning to the Database window. See Chapter 4, "Recipes," and Chapter 8, "Sequencing," for information on using the Recipe and Sequence editors.

9.5 EXPORTING DATA

You can export Scan or Sequence data to floppy diskettes, or to another directory on the instrument computer's hard disk.

Recipe export is not supported in this release. However, if you have the GEM/SECS Option, both data and recipes can be exported by uploading to a host computer. See Section 10.5, "Downloading Data and Recipes," for more information.

You can export data in two formats:

- ASCII format for transferring data to other applications such as spreadsheets, word processors, desktop publishing or presentation software
- Binary format for use on another Tencor P-20h, or for backing up and archiving data in its original format

To export Scan or Sequence Data:

1. Display the Scan or Sequence Data catalog by clicking on the appropriate command button on the left side of the window.
2. Select the recipe you wish to print by clicking or scrolling with the arrow keys.
3. Click on the Export button below the catalog, or the Export button in the tool bar. The following dialog box appears (Fig. 9-7).

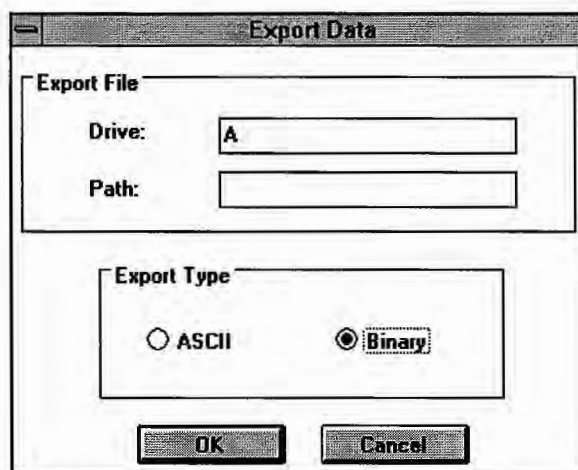


Figure 9-7 Export Data Dialog Box

4. In the Drive field, type a if exporting to a floppy diskette, or c if exporting to another directory on the hard disk.
5. In the Path field, type the desired path name, if any.
6. If a different filename is desired, type it in the Filename field.
7. Choose whether to export the file in ASCII or Binary form by clicking on the corresponding radio button.
8. Click on OK to export the file, or Cancel to close the dialog box without exporting.

9.6 IMPORTING DATA

You can import Scan or Sequence data from floppy diskettes, or from another directory on the instrument computer's hard disk. Data can only be imported in Tencor P-20h binary format.

Recipe import is not supported in this release. However, if you have the GEM/SECS Option, recipes can be imported by downloading from a host computer. See Section 10.4, "Uploading Recipes," for more information.

To import Scan or Sequence Data:

1. Display the Scan or Sequence Data catalog by clicking on the appropriate command button on the left side of the window.
2. Click on the Import button below the catalog, or the Import button in the tool bar. The following dialog box appears (Fig. 9-8).

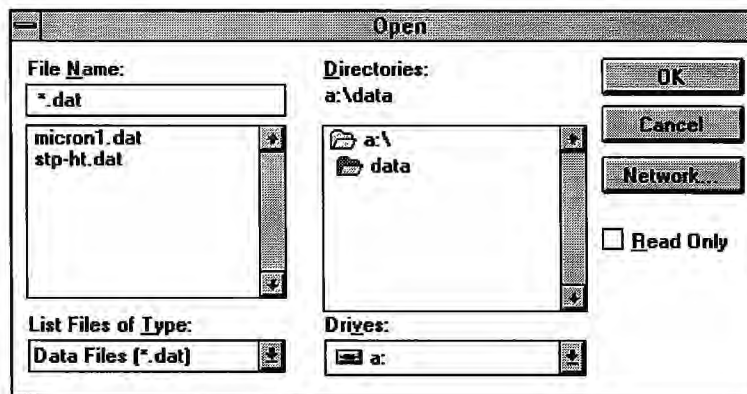


Figure 9-8 Open Dialog Box

3. On the right side of the dialog box, select the drive from the Drives pull-down list, and the directory from the Directories list box.
4. A list of available files with the extension .DAT appears in the list box beneath the File field on the left side of the dialog box. If you want to see a list of files with other extensions, select All Files (*.*) from the List Files of Type pull-down list.
5. Select the desired file, then click on Open. The following dialog box appears:

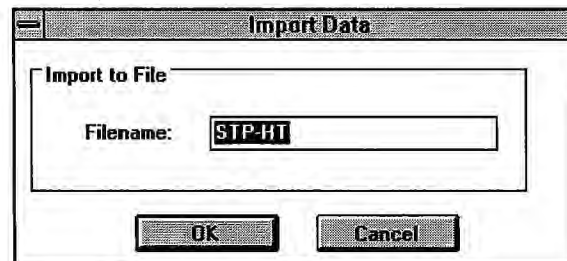


Figure 9-9 Import Data Dialog Box

6. If you want to rename the file, type the desired name; otherwise, leave the default name.
7. Click OK. The file is imported into the default Scan or Sequence data subdirectory.

10 GEM/SECS OPTION

The GEM/SECS Option allows the uploading of scan measurement data from the Tencor P-20h to a host computer. The capability also supports alarms, data collection, equipment states, error messages, initialization, clock, and process program upload and download.

This chapter describes

- The GEM/SECS window
- Enabling SECS communications
- Checking communication status
- Configuring GEM parameters
- Uploading data and recipes
- Downloading recipes

For detailed information about the GEM/SECS Option, see the *Tencor SECS Interface Manual*.

10.1 GEM/SECS WINDOW

To open the GEM/SECS window, use the Top Level menu (Fig. 3-2).

To access the GEM/SECS window:

Click on the GEM+SECS icon in the Top Level menu. The GEM User Interface window appears:

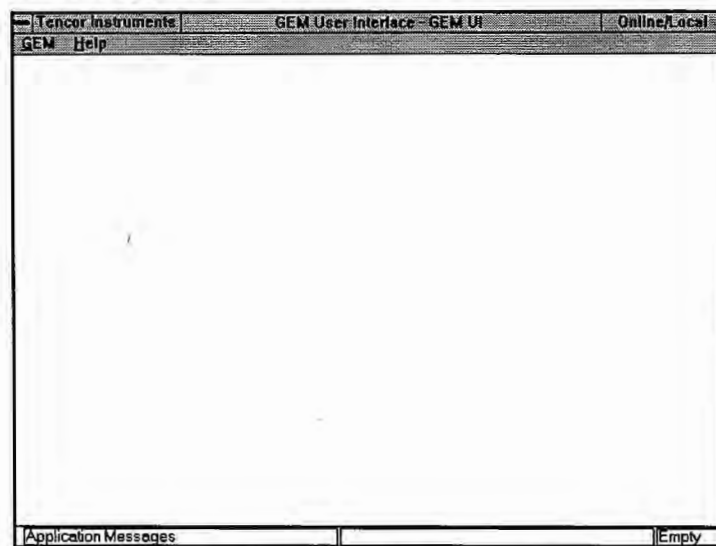


Figure 10-1 GEM User Interface Window

10.1.1 GEM/SECS WINDOW MENU BAR

The GEM User Interface menu bar provides the following menus. You can view menus by clicking on the titles in the menu bar, or by pressing ALT + *I*, where *I* is the letter that appears with an underscore in the desired title in the menu bar. You can choose menu items by clicking on a menu entry or by typing the letter that appears with an underscore in the desired menu item. Some menu items have hot keys assigned to them.



Figure 10-2 GEM File Menu

10.2 ENABLING SECS COMMUNICATION

To enable/disable SECS communication:

Select Enabled from the GEM menu to toggle between states. When communications is enabled, a check appears next to the menu selection.

To check the GEM status:

From any window, the current control state is displayed in the upper right corner of the window in the menu bar. For more complete information, double-click on the displayed control state, and the following message box appears:

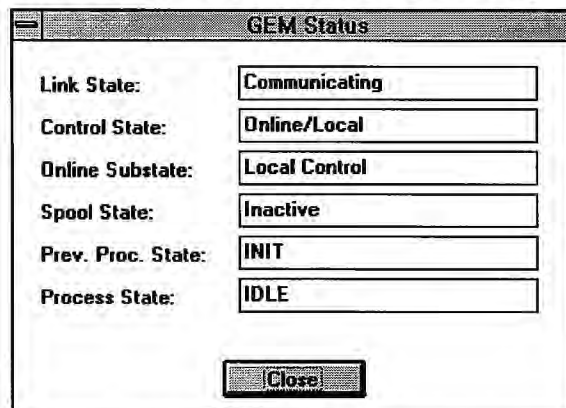


Figure 10-3 GEM Status Message Box

10.3 GEM CONFIGURATION

GEM parameters can be configured by the operator or host. The GEM Configuration dialog box enables configuration of the GEM-related parameters (configuration, initial states, SIF2 message items, optional W-bit use, and host connect retry delay).

To change the default GEM parameters:

1. From the Top Level menu, double-click on the GEM+SECS button. Select Config... from the GEM menu. The GEM Configuration dialog box appears:

GEM Configuration	
Communication Init. Comm. State: <input type="button" value="Enabled"/> Poll Delay: <input type="text" value="15"/> Estab. Comm. Delay: <input type="text" value="20"/>	Control States Init. Control State: <input type="button" value="Online"/> Online Failed State: <input type="button" value="Equipment Offline"/>
Spooling <input checked="" type="checkbox"/> Spooling Enabled <input type="checkbox"/> Overwrite Spool Max. Spool Transmit: <input type="text" value="0"/> Max Spool File Size: <input type="text" value="10000"/>	Event Reports <input type="checkbox"/> Annotated Reports (S6F13) <input checked="" type="checkbox"/> W-Bit for S6
Equipment Identification Model (MDLN): <input type="text" value="P-20"/> Rev.: <input type="text" value="2.2"/> Device Name: <input type="text" value="P-20 PROFILE"/>	Alarms <input checked="" type="checkbox"/> W-Bit for S5
Terminal <input checked="" type="checkbox"/> W-Bit for S10	
<input type="button" value="OK"/> <input type="button" value="Cancel"/>	

Figure 10-4 GEM Defaults Window

2. Change the parameters as appropriate. When finished, click on the OK button. These values are saved to the hard disk so that when the instrument is reset or powered on again, these new values are displayed.

You can also click on Cancel to close the GEM Configuration window without changing the parameters.

10.4 UPLOADING RECIPES

With the GEM/SECS Option, you can *upload* (export) data and recipes to a host computer.

To upload data and recipes to a host computer:

1. From the appropriate catalog window, select the recipe or data set you wish to upload.
2. Select Upload from the PPTransfer menu. The following dialog box appears (Fig. 10-5).

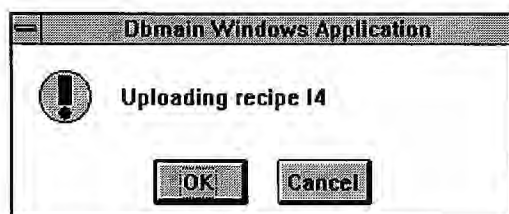


Figure 10-5 Upload Dialog Box

Click on OK to proceed with the upload, or Cancel to abort the operation.

10.5 DOWNLOADING DATA AND RECIPES

With the GEM/SECS Option, you can *download* (import) recipes (but not data) from a host computer.

NOTE: You can import Tencor P-20h data files (in binary format) from floppy diskettes. See Section 9.6, "Importing Data," for more information.

To download recipes from a host computer:

1. From the Recipe or Sequence catalog, select Download from the PPTransfer menu. The following dialog box appears:

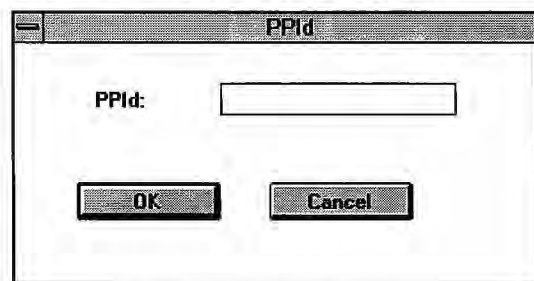


Figure 10-6 PPID Dialog Box

2. Type the PPID of the recipe that you wish to download, then click on OK to proceed. After a few moments, the recipe appears in the list.

11 WAFER STRESS APPLICATION OPTION

11.1 OVERVIEW

It is important to monitor thin film stress so that thin film stress data can be used to reduce process variations. Stress is generated in the film and substrate during thin film deposition. The deformation of the thin film can be accommodated by the bending and compressing or expanding (depending on the curvature) of the substrate.

The Tencor P-20h Wafer Stress application Option enables you to calculate the stress in a deposited film by measuring the wafer deflection or curvature that stress induces on the substrate.

The program determines the curvature of the sample by calculating the least square fit of the trace data. The equation for stress is as follows:

$$\sigma = \frac{1}{6R} \frac{E}{(1-\nu)} \frac{t_s^2}{t_f}$$

where

$$\begin{aligned} \frac{E}{(1-\nu)} &= \text{substrate elastic constant} \\ t_s &= \text{substrate thickness} \\ t_f &= \text{film thickness} \\ R &= \text{radius of curvature} \end{aligned}$$

The program calculates the radius of curvature by using a least square fitting method. This equation assumes that the chord length is much larger than the bow (that is, the wafer deflections are smaller compared to its radius of curvature).

Note: The program results can be verified by using the following equation for the radius of curvature (R):

$$R = \frac{L^2}{8B}, \text{ if } L \gg B$$

where

$$\begin{aligned} B &= \text{bow (maximum between trace and its chord)} \\ L &= \text{chord length (scan length)} \end{aligned}$$

Note: Geometric dimensions are in the same units.

The Tencor P-20h program calculates the following stress values:

- Average Stress derived from the least square fit of the entire profile across the entire chord
- Maximum Stress based on the maximum of n overlapping sections of one-third of the length and offset across the wafer, where n is a number selected by the user
- Center Stress computed at the center third of the profile

11.2 USING THE WAFER STRESS APPLICATION

Use the Wafer Stress application to compare pre- and postprocessing traces. This comparison calculates the curvature caused solely by the processing-induced stress. For details see Section 11.6.1, “Measuring a Difference Stress.”

You also can take a single stress measurement without comparing it to an earlier measurement. You may want to take this measurement when you have no prestress data for a wafer. For details see Section 11.6.2, “Measuring a Single Trace Stress.”

Only the pre- and poststress traces and summaries are saved. Stress values are not saved but recalculated each time from the raw traces. To recalculate the stress values, both the pre- and poststress traces must be present in the Scan Data catalog.

11.2.1 ENTERING SCAN IDS

You enter a name for each scan that you take. You can use any given scan for either the pre- or the postscan.

For example, if you have a two-process step and take three scans, the middle scan is the postscan for the first scan, but it is the prescan for the second scan.

11.2.2 SAVING DATA

To recompute and display difference measurements, both pre- and poststress raw data must be saved. Also, saving the raw and summary data allows you to recalculate the stress value with different parameters.

11.3 THE STRESS WINDOWS APPLICATIONS

To access Tencor’s Wafer Stress application, click on the Stress icon on the Top Level Menu of the P-20h Profiler. The Stress Windows Applications screen displays, as shown below.

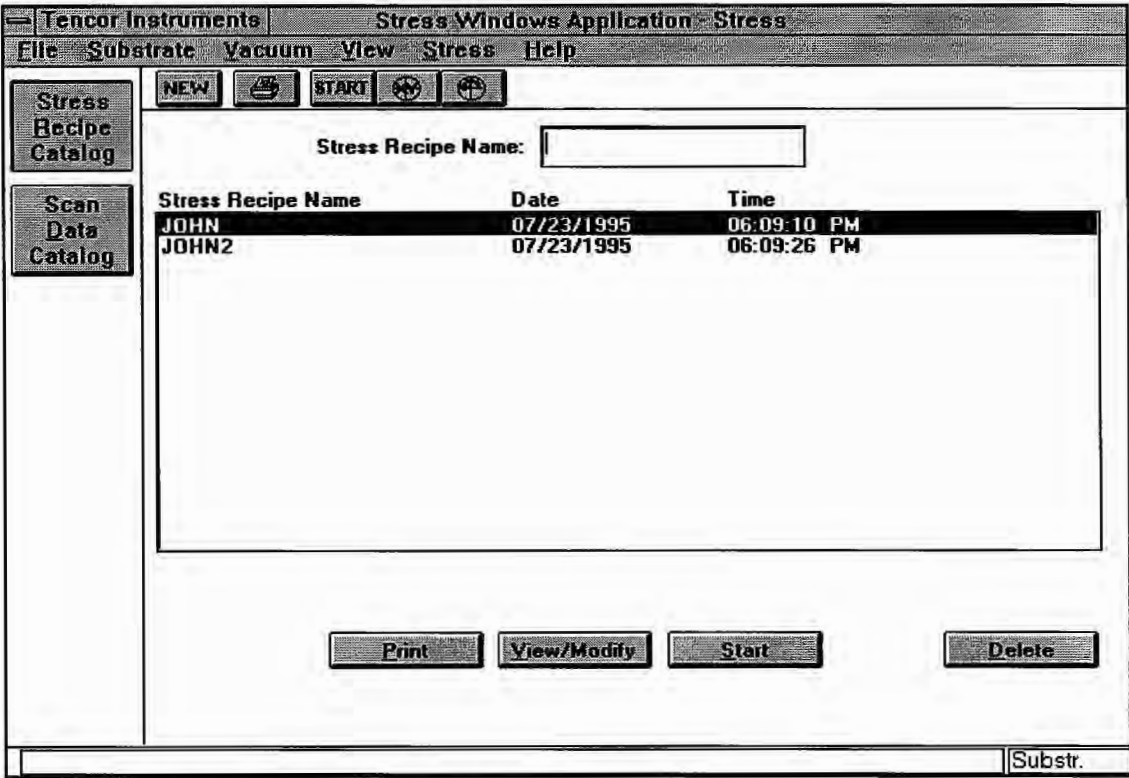


Figure 11-1 Stress Windows Application Screen

The Stress Windows Application screen provides you with two catalogs of stress recipes and scan data. The Stress Recipe Catalog lists the currently available stress recipes saved on the hard disk by name and date. The Scan Data Catalog lists the existing scans saved on the hard disk by scan ID, stress recipe used, X-, Y-coordinates of the scan, and the date and time the scan was taken.

11.3.1 STRESS WINDOWS APPLICATION MENU BAR

The Stress Windows Applications menu bar provides the following menus:

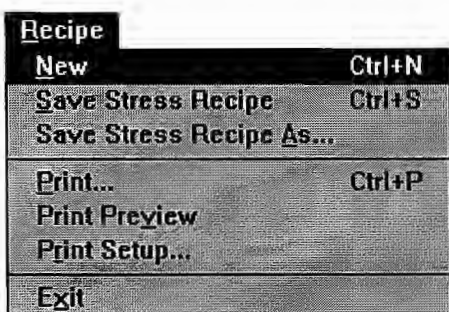


Figure 11-2 Recipe Menu

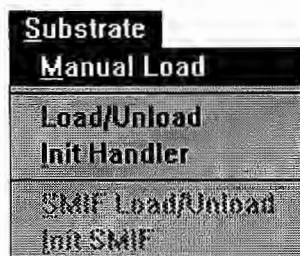


Figure 11-3 Substrate Menu



Figure 11-4 Vacuum Menu



Figure 11-5 View Menu

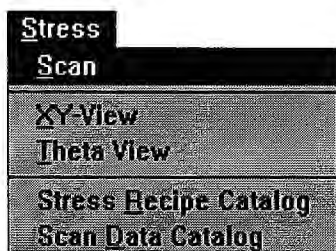


Figure 11-6 Stress Menu

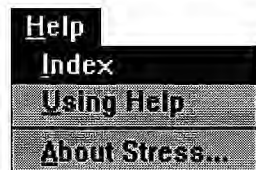








Figure 11-7 Help Menu

11.3.2 STRESS WINDOWS APPLICATIONS TOOL BAR

The Stress Windows Application tool bar contains a row of icons that resemble buttons. Clicking on these icons provides an alternative way to access commonly used functions.

Button	Action
	Invokes the Stress Recipe Editor to add a new stress recipe.
	Displays the Print dialog box to print data for the current page.
	Starts a scan using the current recipe.
	Switches to the XY view window.
	Switches to the Theta view window.
	Shortcut key to save changes to the current file.

11.4 SELECTING, MODIFYING, AND ADDING A SCAN RECIPE

To select a recipe:

Click on the Stress Recipe Catalog of the Stress Windows Application screen. A list of available recipes displays in a list box, as shown in Figure 11-8. Select an existing receipt from this list.

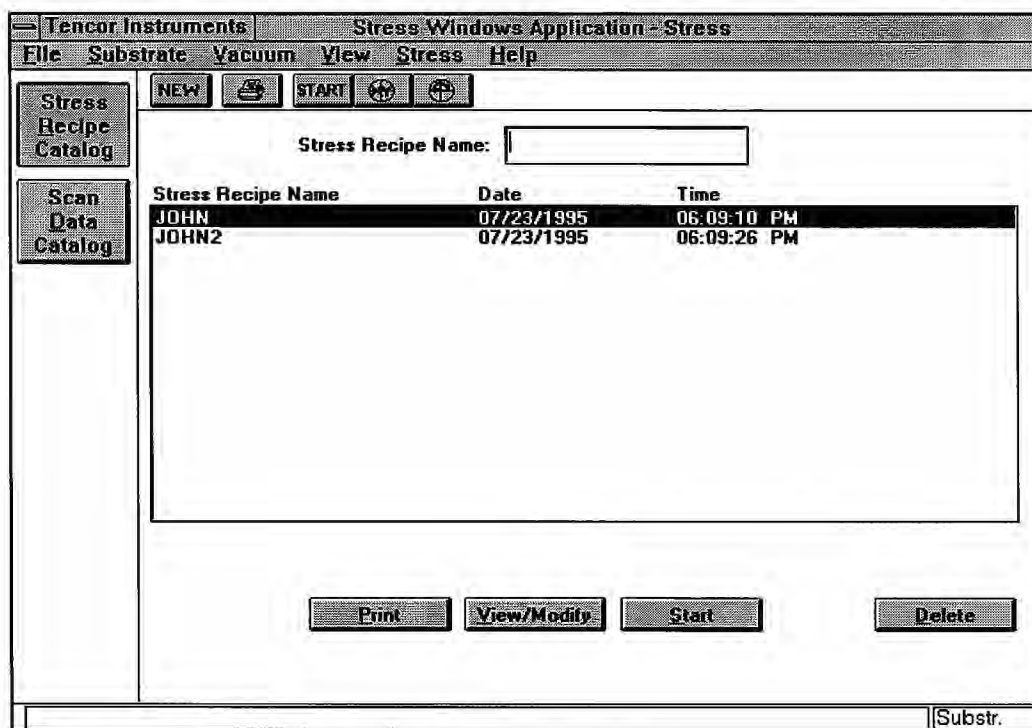


Figure 11-8 Stress Recipe Catalog

To modify a recipe:

Once you have selected a recipe from the Stress Recipe Catalog, you can edit that recipe by selecting the View/Modify button to invoke the Stress Recipe Editor screen (Figure 11-2).

Tencor Instruments Stress Windows Application - Stress

File Substrate Vacuum View Stress Help

NEW [Save] START [Stop] [Reset]

Stress Recipe

Stress Recipe Name: JOHN

Stress Points: 15

Substrate Specification:

Name: 1.239 Gallium Arsenide 100

Thickness: 1000 um

Modulus: 1.239 x10¹¹ Pa

Origin

X: 0 um Y: 0 um

Scan Parameters

Scan Length: 1500 um Sampling Rate: 200 Hz

Scan Speed: 100 um/s Stylus Force: 5.0 mg

Substr.

Figure 11-9 Stress Recipe Editor

To add a new stress recipe:

From the Stress Windows Application screen choose the View/Modify button. At the Stress Recipe Editor screen click on the New button to start writing the new recipe.

To print a stress recipe:

Click on the Print button to print the currently selected stress recipe.

To save a stress recipe:

To save the currently selected stress recipes, select the Save Stress Recipe menu item from the File menu. Use the ESC key to return to the Stress Windows Applications screen. The XY button switches to the learning mode.

11.4.1 ENTERING STRESS RECIPE VALUES AND PARAMETERS

There are several fields in the Stress Recipe Editor window that you need to enter to complete writing a new recipe. Among these values, you need to enter the film thickness and specify the substrate for the sample.

To enter stress parameters:

1. In the Thickness field, type the thickness (in microns) of the substrate.
2. In the Substrate Specification field, select a desired substrate with its elastic constant. Table 11-1 lists the available substrates and their elastic constants.

Table 11-1 Elastic Constants for Commonly Used Thin Film Substrates

Material	Orienta- tion	Elastic Constants (10^{11} Pa)
Aluminum	*	1.030
Aluminum Oxide (Al_2O_3)	+	3.835
Aluminum Oxide (Al_2O_3)	+	4.895
Aluminum Nitride (AlN)	+	4.367
Beryllium Oxide (BeO)	+	4.367
Borophosphosilicate (BPSG) glass	+	1.500
Gallium Arsenide (GaAs)	111	1.741
Gallium Arsenide (GaAs)	100	1.239
Germanium (Ge)	111	1.837
Germanium (Ge)	100	1.420
Phosphosilicate (PSG) glass	+	0.988
Silicon	111	2.290
Silicon	100	1.805
Sodalime glass (Corning microsheet 0211)	+	0.973

* polycrystalline

+ amorphous

<Other> Allows the user to enter a substrate that does not exist on the list.

11.5 LOADING AND POSITIONING THE SAMPLE

For information on loading and positioning the sample, refer to Section 5.2, “Loading a Sample,” and Section 5.3, “Viewing and Positioning the Sample.” Before loading a sample, check that it meets the following requirements:

- The sample has been processed.
- It was scanned before the processing.
- The scan is in the database.

To position the sample to measure stress by comparing pre- and postprocessing traces:

NOTE:	Position the sample exactly as it was positioned for measuring stress on a single trace scan.
--------------	--

1. Use the wafer stress precision locator, which is the locator with the three support points. Be sure that you position the sample the same way it was positioned for the prestress scan.

NOTE:	If you are using the wafer handler to load wafers, make sure the wafer stress locator is installed on the stage before starting stress measurements. See below for details. See Section 11.5.1, “Tencor P-20h Handler Wafer Stress locator.”
--------------	---

The precision locator has fittings that locate wafers of various sizes in X, Y, and θ positions. It supports the wafers in a way that minimizes gravitational distortions but also ensures that the residual gravitational distortion is the same for both pre- and poststress scans.

2. You can program the instrument so that the load position moves the stage to exactly the right scan position. See Section 5.2, “Loading a Sample.”

11.5.1 TENCOR P-20H HANDLER WAFER STRESS LOCATOR

The wafer stress locator (Figure 11-10) is designed to support the wafer during wafer stress measurements. The instrument is shipped with the vacuum chuck installed if your instrument comes with the wafer handler. To replace the vacuum chuck with the wafer stress chuck, use the instructions provided in Section 2.5, “Installing a Precision Locator,” in the *Tencor P-20h Long Scan Profiler Reference Manual*.

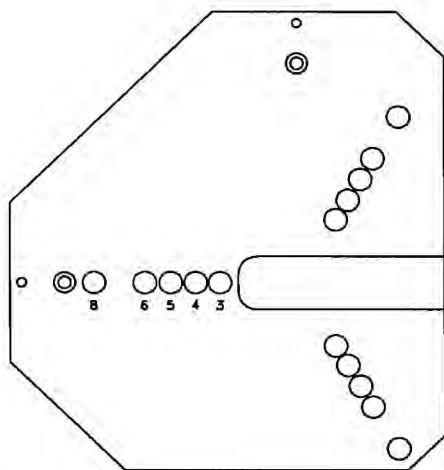


Figure 11-10 Wafer Stress Locator

The handler controls the placement of the wafer by centering it on the locator. The three wafer support pins can be located for wafers of nominal sizes 3 to 8 in. See Appendix D, "Precision Locators," in the *Tencor P-20h Long Scan Profiler Reference Manual*.

- If the wafer is loaded using the wafer handler, make sure the wafer is loaded using the aligner. Also the angle used for alignment must be the same for the prestress and poststress loading.
- If the sample is loaded manually, note the position of the sample when you load it on the stage table. To compare pre- and poststress measurements, you must duplicate this scan position for the poststress measurement.

11.5.2 TAKING A SCAN

A single poststress measurement measures the current curvature of the sample. In its calculations, the program assumes that the sample was flat before being stressed.

To take a single, poststress measurement:

1. Load the sample.
2. Choose a recipe from the list box (or create a new recipe).
3. Position the sample for the scan.
4. Display either the Stress Windows Applications screen or the Stress Recipe Editor screen if you are modifying an already existing recipe or creating a new recipe.
5. Enter film and substrate information for the sample.
6. Select START either from the Stress Windows Applications screen or from the Stress Recipe Editor screen.

11.5.3 DISPLAYING A LIST OF SCANS

Selecting the Scan Data Catalog button of the Stress Windows Application screen displays a list of currently existing data scans on the hard disk by scan ID, scan recipe used, X-, Y-coordinates of the scan, and the date and time the scan was generated. The Scan Data Catalog is shown in Figure 11-11.

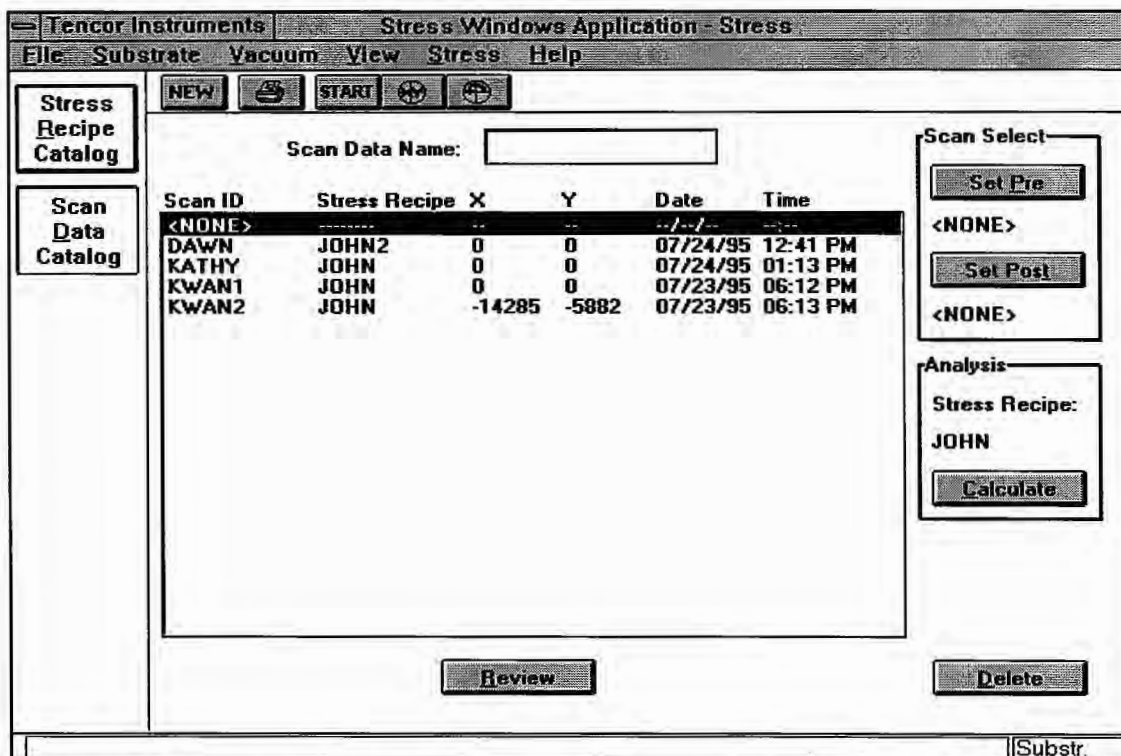


Figure 11-11 Scan Data Catalog Screen

You can remove a scan from this list simply by selecting the scan, then selecting DELETE. Pressing ESC while in this screen takes you back to the Stress Windows Application screen.

11.5.4 VIEWING SCAN RESULTS

The Stress application provides you with two ways to access the Scan Results window (Figure 11-13) to view a particular scan without performing analysis on the scan.

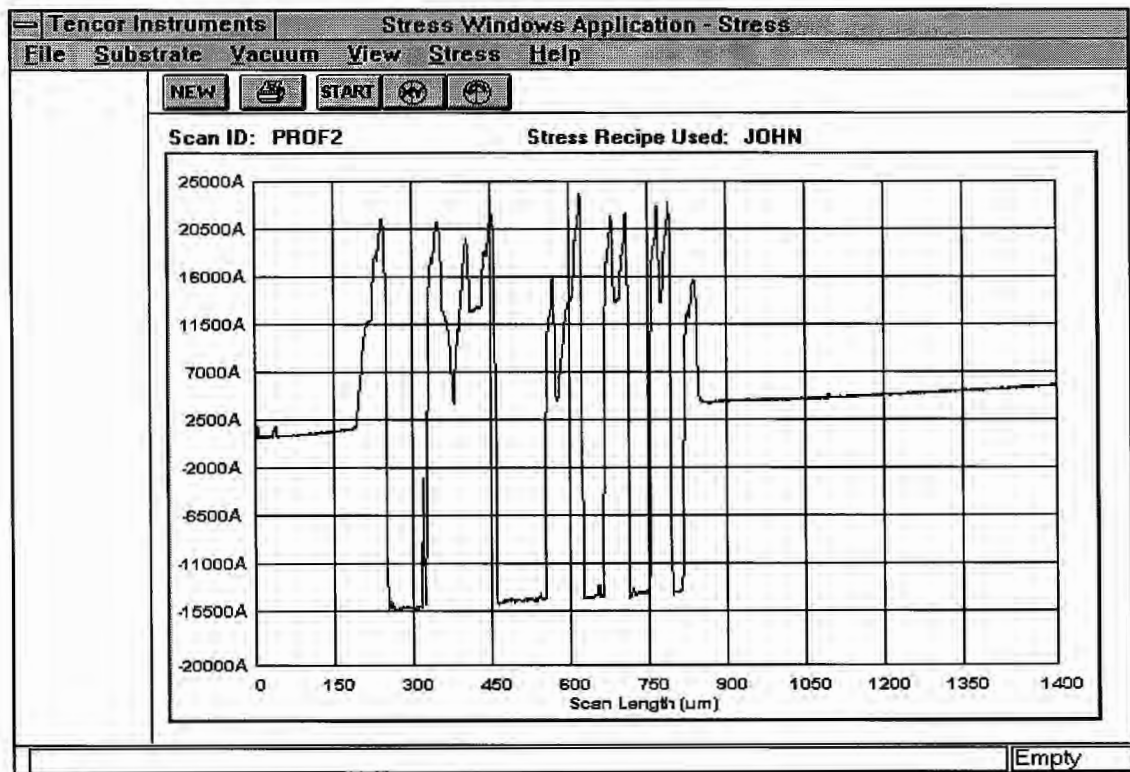


Figure 11-12 Scan Results Window

To view scan results from the Stress Recipe Catalog:

1. Select START from the tool bar to perform a scan, which will be displayed at the finish.
2. Press ESC on the keyboard to return to the Stress Recipe Catalog screen where you can start another scan.

To view scan results from the Scan Data Catalog:

1. Select the desired scan from the selected a particular scan, select REVIEW to display the scan.
2. Use the ESC key to return to the Scan Data Catalog screen.

11.6 ANALYZING THE STRESS RESULTS

You can calculate both a *poststress* measurement on a single trace and a *difference* measurement, which compares the poststress data in the current trace with prestress data from an earlier scan.

11.6.1 MEASURING A DIFFERENCE STRESS

The Stress application enables you to perform analysis on pre- and postprocessing traces. To accomplish this, you need to assign a particular scan of your choice that you select from the list box as a prestress scan and then select another scan from this list and assign that scan as the poststress scan.

To measure a difference stress:

1. To assign scans as prescan and postscan, use the Stress Windows Application screen (Figure 11-13).

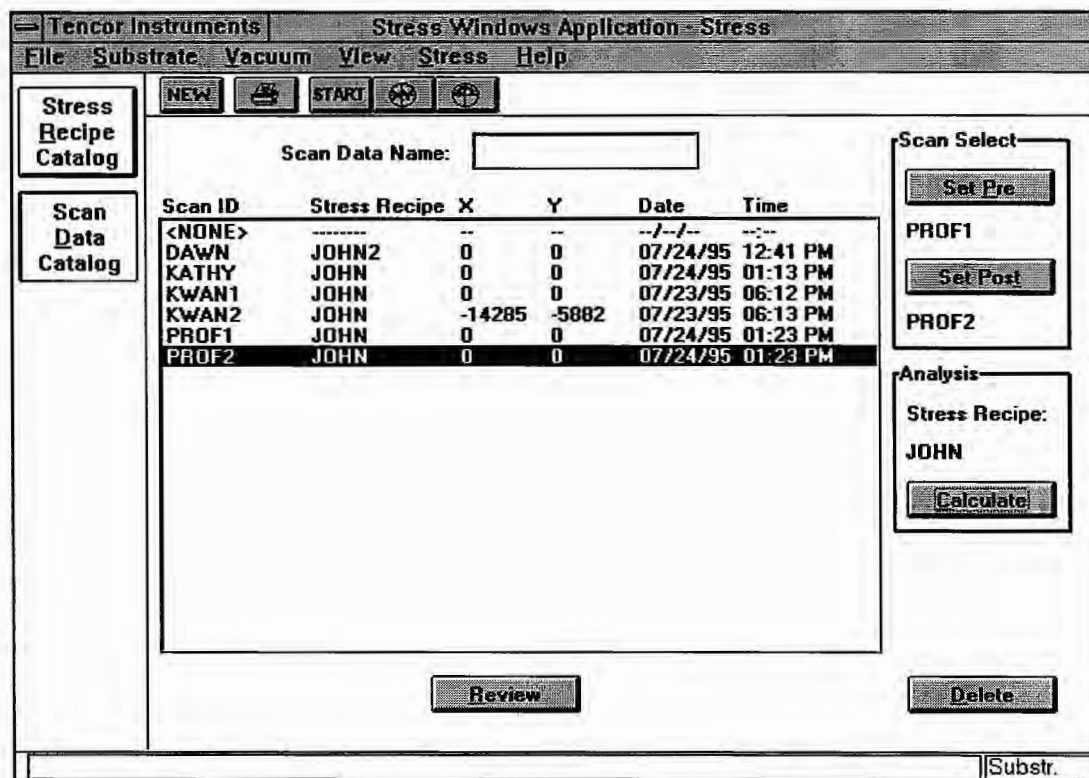


Figure 11-13 Stress Windows Applications

2. Select the Scan Data Catalog button.
3. Select a scan from the list box or enter a scan name in the Scan Data Name field.
4. Select SET PRE to assign that scan as a prestress scan.
5. Similarly, select another scan from the list box.
6. Select SET POST to assign that scan as the poststress scan.

Note: As you make these assignments, notice that the scan ID of the scan you have selected appears below the SET PRE and SET POST buttons.

- After selecting the two scans, select CALCULATE to calculate and view the results (Figure 11-14).

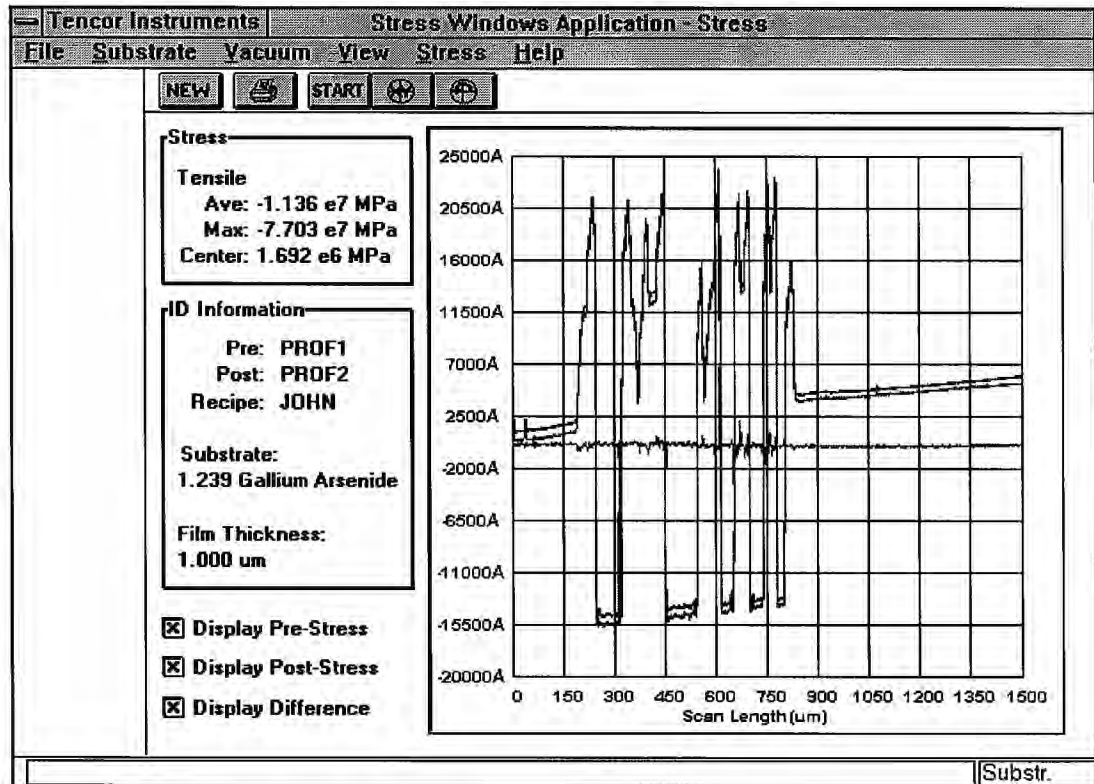


Figure 11-14 Stress Results Display

11.6.2 MEASURING A SINGLE TRACE STRESS

In addition to comparing pre- and poststress processing traces, you can take a single stress measurement without comparing it to an earlier measurement. You may want this measurement if you do not have, or choose not to use, prestress data for a wafer.

To measure a single trace stress:

- Select the NONE scan ID from the Scan Data Catalog list box (the first choice in the box).
- Select CALCULATE on the Scan Data Catalog screen to calculate and view the results on the Stress Recipe Display screen.

11.6.3 ANALYZING THE RESULTS

The Stress Results Display (Figure 11-13) lets you display the Prestress, Poststress, and Difference deflections. Each of these traces has a corresponding check box labeled Display Pre-Stress, Display Post-Stress, and Display Difference.

The Stress Results Display shows the three traces in three different colors. If you have not specified a prestress trace, that line appears as a flat line.

This screen also displays the results of the calculation (Figure 11-14) as well as the IDs of the prestress and poststress scans and the stress recipe name used.

NOTE:	If you specify two scans by using different scan recipes, the Stress application calculates the stress by giving the best estimate over the region where data is available for both scans. For regions with conflicting sets of data, the program displays a zero stress.
--------------	--

12 SIGNAL LIGHT TOWER OPTION

12.1 OVERVIEW

A Signal Light Tower is a highly visible indicator of a tool's status. The multi-light device can be used to signal that an instrument is in production or to indicate the reason that it is not in production.

The implementation of the Signal Light Tower Option available in the current release of the Tencor P-20h allows you to specify tower responses to specific instrument states. This approach involves some relatively simple hardware and new Profiler software that translates instrument statuses into commands to the new hardware.

12.2 ACCESSING SIGNAL LIGHT TOWER

To invoke the Signal Light Tower window, click on the Configuration icon of the Top Level menu of the P-20h Profiler software. The Configuration window display appears (Figure 12-1).

Handler Load Pos.		Manual Load Pos.	
X :	-98657 μm	X :	2521 μm
Y :	360 μm	Y :	96638 μm
Theta :	2. deg	Theta :	6. deg
Elevator:	47693 μm	Elevator:	28132 μm

Soft Home Theta :	6. deg
Lowest Elevator Position:	55172 μm
Leveling Offset:	0 arc sec
Elevator focus speed:	10

Substr.

Figure 12-1 Configuration Window

12.2.1 SYSTEM CONFIGURATION

A check box has been added to the Configuration window, entitled "Signal Tower." When this button is pressed, the Signal Light Tower Configuration Editor Utility window appears (Figure 12-3).

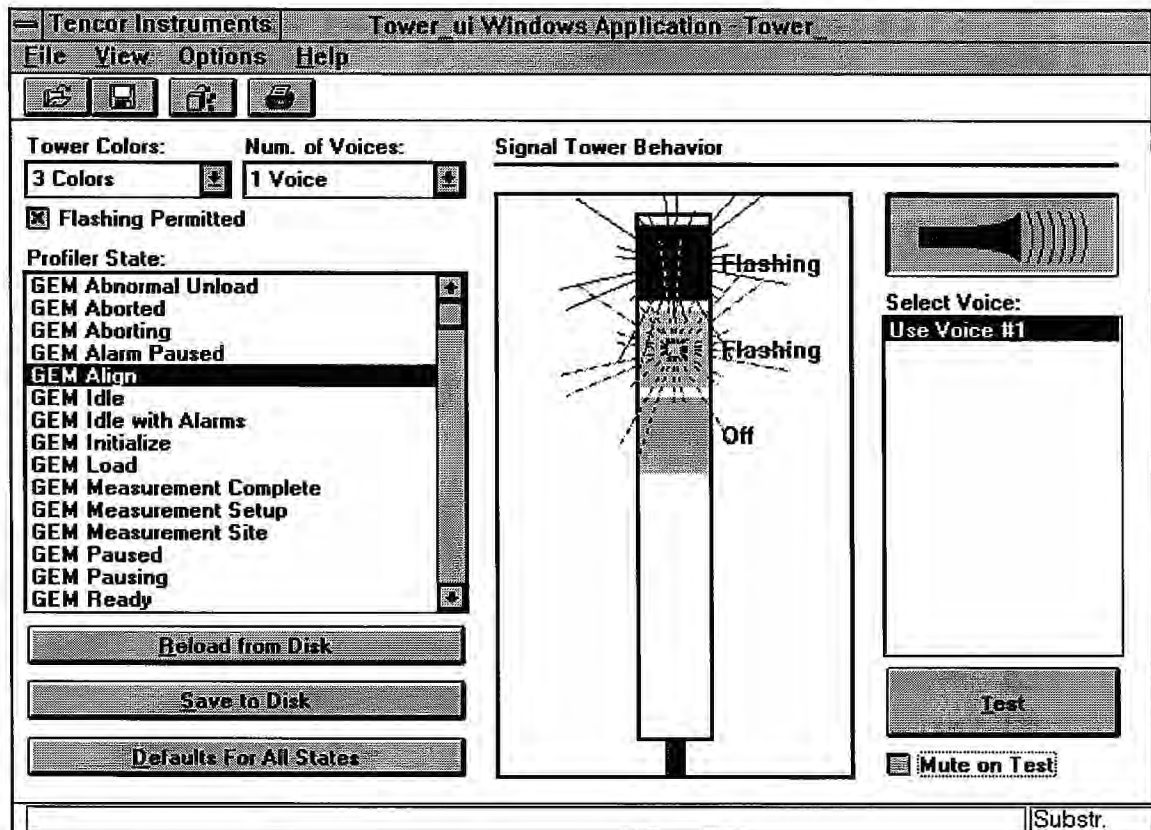


Figure 12-3 Signal Light Tower Configuration Editor Window

12.2.2 SIGNAL TOWER WINDOWS APPLICATION MENU BAR

The Signal Tower Windows Applications menu bar provides the following menus:

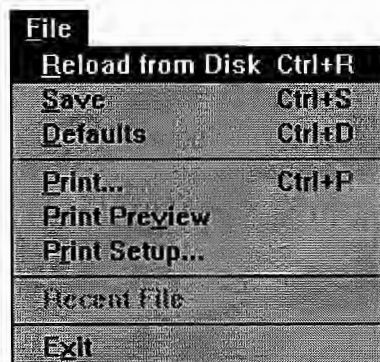


Figure 12-3 File Menu



Figure 12-4 View Menu



Figure 12-5 Options Menu

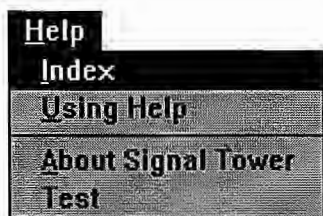


Figure 12-6 Help Menu

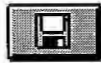
12.2.3 SIGNAL TOWER WINDOWS APPLICATIONS TOOL BAR

The Signal Tower Windows Application tool bar contains a row of icons that resemble buttons. Clicking on these icons provides an alternative way to access commonly used functions.

Button	Action
--------	--------



Load all states. Equivalent to the Reload from Disk button.



Save the changes to all states. Equivalent to the Save to Disk button.



Return all states to factory default settings. Equivalent to the Defaults for All States button.



Displays the Print dialog box to print current states and definitions.

12.2.4 LIGHTING OPTIONS

The Signal Light Tower allows you to specify any of the five lights: red, yellow, green, blue, and white. You can set these lights independently of each other. Lights can be turned off, constantly on, or set to flashing. All lights can be turned off or cleared simultaneously. The tower displays the proper behavior as appropriate for the settings that are current for that Profiler state (Figure 12-3).

You can edit the tower behavior by using the mouse. If you click on a given light, the light toggles its state. This means that if the light was off, it goes to flashing next. If the light was flashing, it goes to on next. If the light was flashing, it turns off any other light since this control prevents illegal behavior such as two lights being on at the same time.

To reach the state where all lights are set to off, click on a blank space, away from any light or just go to the light that is on and toggle its state until the light is off.

12.2.5 LIGHTING EXAMPLES

The following is a list of examples for lighting corresponding to the instrument states.

Light	Description
Red, flashing	Indicates failure, abort, immediate assistance is required.
Red, steady	Indicates the equipment is not fully capable. An alarm has been acknowledged but not corrected.
Yellow, flashing	Indicates that the alarm is not acknowledged and needs assistance, for example, during unload cassette, completion or run, PM, and so on.
Green, flashing	Indicates the equipment is capable of performing all functions but no product is running.
Green, steady	Indicates that the equipment is fully capable and is running wafers.

12.2.6 VOICE OPTIONS

The voice custom control is a two-state button (Figure 12-3). It toggles between on and off. When voices are permitted and it is in the *on* state, an appropriate picture shows a speaker with sound waves.

When the voice option is in the *off* state, another picture shows a speaker without sound waves.

If sounds are not permitted by the current tower, the button shows the alarm clock with a red X across it indicating that there is no sound capability.

The choices for the number of voices are NONE, and 1 through 16. NONE specifies towers without sound capabilities.

12.2.7 STATUS INFORMATION

Selected portions of the current status of the P-20h profiler are always available to the Signal Light Tower control software. This part of the software informs the user of any changes in the status of the instrument at the time the changes occur.

The list box on the Signal Light Tower window contains a descriptive list (Figure 12-3). You can edit the behavior of the signal tower for a particular state by selecting that state from the list box. At that point, the current behavior for that state is shown with two custom controls, one for the tower voice and one for the tower lights.

You can test a state after editing it by selecting the Test button. This action immediately places the tower into that state so that you can see and hear what the state appears like.

You can then proceed and edit other states by selecting them from the list box and edit them as shown above.

Once you have completed editing the behavior of a state, you can select the Save to Disk button to save the settings for that state. You can cancel the changes to the states by selecting the ESC key and leaving the application without saving to the disk. After you have already saved the changes to the states, you can undo the changes by selecting the Defaults for All States button that returns all states to factory defaults.

You are then prompted for a password, if you have set any. If the password that you enter is invalid, the changes to the state cannot be saved.

The system initially starts with *Welcome* as the password the first time it is run.

GLOSSARY

2D Data

Two-dimensional data.

3D Data

Three-dimensional data.

ASCII Data

ASCII (American Standard Code for Information Exchange) codes are used to represent characters for storage in a computer's memory.

Application

A software program such as the Tencor P-20h Scan application.

Application icon

Graphic symbol representing a software application. The Tencor P-20h Top Level menu displays application icons.

Application window

The main window opened by an application.

Area

See Total Area.

Area+

See Area of Peaks.

Area-

See Area of Valleys.

Area of Peaks (Area+)

Total area bounded by the leveled baseline and the profile above the baseline.

Area of Valleys (Area-)

Total area bounded by the leveled baseline and the profile below the baseline.

Arrow keys

The arrow keys on the operator keypad. These keys can be used to highlight a menu item or dialog box option or to move a text or graphics cursor.

Average Height (Avg)

The average height of all data points between the measurement cursors relative to the leveled baseline.

Avg

See Average Height.

Back up

To save data from the Tencor P-20h hard disk to diskettes or a network drive (if available). The data can be restored at a later time.

Base

Used (with prefix Up- or Down-) to identify the bottom of the sloping side of a step, to distinguish it from the top of the slope, called the *edge*. See UpBase, DownBase.

Bearing Ratio (t_p)

A reference line is drawn parallel to the mean line and at a preselected or predetermined distance (cutting depth) below the highest peak of the roughness trace within the sampling length. This reference line intersects the roughness trace in one or more subtended lengths. The bearing length is the sum of these subtended lengths. The bearing ratio is the ratio of the bearing length to the sampling length. Also called Bearing Length Ratio.

Centerline

The center-line divides the profiles such that all areas above it are equal to all areas below it.

Choose

To pick a menu item or other item that starts an action. You can choose an item using the mouse or keypad.

Click

Pressing and releasing the left or right mouse button without moving the mouse. Clicking the left button on a menu title, on an icon, on a dialog box option or command button, or in a window selects the item. Left and right buttons have different functions when clicking. *Compare to* double-click.

Concave

Describes an arc that curves inward from a level reference plane; a valley-like arc.

Contact Speed

Contact speed defines the stylus drop speed at contact with the substrate.

Convex

Describes an arc that curves outward from a level reference plane; a hill-like arc.

Cursor

An object on the screen that can be moved with the mouse or arrow keys and that allows the user to locate or edit data. *See* limit cursor, particle cursor, and text cursor.

CutDp

See Cutting Depth.

Cutoff Length

The cutoff length is the wavelength on the filter transmission curve that corresponds to 75% transmission. According to the ANSI B46.1-1985 standard, 800 μm is the preferred cutoff for most surfaces.

Cutting Depth (CutDp)

A preselected or predetermined distance below the highest peak of a sample. *See* Bearing Ratio.

 D_q

See Root-Mean-Square Slope.

Database

A collection of data organized by records. The Tencor P-20h database can contain data summaries, maps, user IDs, system log records, recipe records, and other data.

Deskew

Deskew is a feature of the Tencor P-20h that compensates for any translational or rotational errors between different substrates by allowing you to select manually two fixed reference points to be used for calculating stage coordinate values.

Dialog box

A rectangular box on the screen that can contain a combination of lists, options, data entry fields, and command buttons. A dialog box appears when the instrument needs more information before performing an operation.

Disk space

The total amount of space available on the hard disk. Free disk space is the amount of disk space unused.

Directory

Computer files are stored on the computer's hard disk in directories. The directory name identifies the location where the files are stored. *See* Path.

Download

Importing a recipe from a remote host through the GEM/SECS Option.

DOS

Disk Operating System, also called MS-DOS. The central program used to control and manage the computer system.

Double-click

The mouse action performed when you press and release the mouse button twice in rapid succession. The first click selects the item and the second click performs the action associated with the item. When you double-click the left button on an application icon, the application starts. Left and right buttons have different functions when double-clicking. *Compare to* click.

DownBase

The bottom of the sloping side of a trough-like feature, or downward step.

DownEdge

The top of the sloping side of a trough-like feature, or downward step.

Drag

The mouse action performed when you hold down the mouse button and move the mouse. Dragging can be used to choose a menu item and to move a graphics cursor.

Drive (disk)

The disk drive identifier. A single character followed by a colon. For example, C: refers to drive C.

Edge

The distance to the first rising or falling edge of a step (or the apex of a peak) from the beginning of the profile. Also used (with prefix Up- or Down-) to identify the top of the sloping side of a step, to distinguish it from the bottom of the slope, called the *base*. See UpEdge, DownEdge.

Export

To save selected data, such as recipes, wafer summaries, and wafer maps, to diskette. Exported data can be imported into another Tencor P-20h system. *See* import.

Field

A rectangle in a dialog box used for entering data. The text cursor (a vertical bar) generally appears in the first field in a dialog box.

Finite Impulse Response (FIR)

The Tencor P-20h uses the Finite Impulse Response technique to calculate roughness and waviness from digitized data points.

Form Error

Form error is a deviation from a perfect realization of a nominally specified shape. For example, for a flat surface the form error would be the deviation from flatness. If the deviation is periodic (that is, has waves), the error is termed waviness. If there are many hundreds or thousands of randomly shaped undulations without a discernible pattern, the error is called roughness. The difference between form error, roughness, and waviness is not precisely defined; it is more a qualitative distinction. *See* Waviness and Roughness.

GEM

Acronym for *Generic Equipment Model*.

Graphics cursor

Graphics cursors appear as vertical bars in histogram windows and can be used to change defect bin splits.

HSC

See High Spot Count.

Height

The difference in height between two points on the sample surface defined by the positions of the measurement cursors.

High Spot Count (HSC)

The number of profile peaks per unit length projecting through a reference line parallel to and at a given height above a line drawn through the lowest point of the roughness trace, parallel to the mean line. See Peak Count.

Import

To load data previously saved in an export file. *See* export.

Keylock

The keylock limits operator access to Scan recipes and Sequence programs for operational security.

 L_q

See Root-Mean-Square Wavelength.

Locator

The plate upon which a cassette rests when on the handler. The locator must be changed for different cassette sizes.

Log Off

Sign off from the Tencor P-20h by choosing the Log Off icon from the To Level menu.

Manual/Single Scan Mode

The user programs the parameters for a scan into a recipe using a menu. The scan can be specified to be continuous or segmented into sections of equal length.

Maximum Height (MaxHt)

The maximum height of a trace relative to the zero line within the sampling length.

Max R_a

See Maximum Average Roughness.

Maximum Average Roughness (Max R_a)

The trace within the cursors is divided into 19 overlapping sections. Each section is one-tenth of the sampling length. The average roughness (R_a) of each section is calculated and the maximum is displayed.

Maximum Stress

Maximum stress is the maximum of 13 overlapping sections of one-third the length and offset across the total profile.

Mean Peak Height (Rpm)

The mean value of the local peak heights of the roughness trace within the sampling length.

Mean Peak Spacing (S_m)

The mean value of the local peak spacing of the roughness trace within the sampling length, where the peaks are defined by the criteria of the Peak Count parameter. *See* Peak Count.

Menu

A list of commands. Two types of menus are supported — icon-based menus and drop-down menus. Full-screen menus such as the Top Level Menu display application icons. You can start an application by double-clicking the left button on its icon. A menu in the menu bar opens when clicked. *See* menu bar.

Menu Bar

Menu bars are displayed at the top of application windows and list menu titles. You can open a menu listed in the menu bar by clicking on its title. You can choose from the menu by clicking on an item.

Microsoft Windows

A graphical user environment developed by Microsoft Corporation that uses windows to present information and a pointing device, usually a mouse, for user interaction.

Minimum Height (Min Ht)

The minimum height of a trace relative to the zero line within the sampling length.

Multiscan Average Mode

A scan is repeated up to ten times and the average is calculated automatically.

PC

See Peak Count.

Parameters

Measurement attributes such as length, speed, and direction are the parameters used in the Tencor P-20h software.

Path (to file)

The location of a file or directory. A complete path consists of a drive identifier (A:, for example) followed by the directory and subdirectory names. The directory and subdirectory names are separated with the backslash character (\). In C:\DATA\TEMP\TEST.DAT, the path to the TEST.DAT file is C:\DATA\TEMP.

Peak

The distance between the mean line and the highest peak of the roughness trace or waviness trace within the sampling length.

Peak Count (PC)

The number of peak/valley pairs in the roughness trace per unit length, projecting through a band of width b , and centered about the mean line. Projecting through means that the profile curve climbs above and then falls below the band. Thus, if the profile rises above the band more than once without falling below the band, multiple peaks are not identified. *See High Spot Count.*

Peak/Valley

The vertical distance between the highest peak and the lowest valley of the roughness or waviness trace, leveled on the mean line. Also known as R_{\max} or W_{\max} , Maximum Peak-to-Valley Roughness or Waviness.

Profile Length (Profl)

The length that would be obtained from drawing out the profile in a straight line within the sampling length.

Profl

See Profile Length.

 R_{3z}

See Six-point Height.

 R_a

See Roughness Average.

 R_h

See Roughness Height.

 R_p

See Peak.

 R_q

See Root-Mean-Square Roughness.

 R_t (P/V)

See Peak/Valley.

R_v

See Valley.

R_z

See Ten-Point Height.

RMS

See Root-Mean-Square.

Rpm

See Mean Peak Height.

RRWG

Acronym for raw scan, roughness, waviness, and grid. The RRWG colors represent the individual color options for the graph and grid lines.

Radius

The distance from the center of curvature of the profile arc (assuming a circular profile within the sampling length) to the profile. The measurement cursors define two points of a circular arc. A least squares fit is performed on the points between the cursors.

Recipe

A recipe is a list of scan parameters.

Recipe ID

The Recipe ID is the name of the generating recipe.

Restore

To return data previously saved by a backup operation.

Root-Mean-Square Roughness (R_q)

The root-mean-square or geometric average deviation of the roughness profile from the mean line measured in the sampling length.

Root-Mean-Square (RMS)

The square *root* of the arithmetic *mean* of the *squares* of a set of numbers.

Root-Mean-Square Slope (D_q)

The root-mean-square or geometric average deviation of the slope of the roughness trace.

Root-Mean-Square Wavelength (L_q)

2π times the ratio of the root-mean-square deviation of the profile (R_q) to the root-mean-square slope of the profile (D_q). L_q is a measure of the spacing of local peaks and local valleys, taking into account their relative amplitudes and individual spatial frequencies.

Root-Mean-Square Waviness (W_q)

The root-mean-square or geometric average deviation of the waviness profile from the mean line measured in the sampling length.

Roughness

A surface is said to be rough when the surface's deviation from flatness has many hundreds or thousands of randomly shaped undulations. *See* Form Error and Waviness.

Roughness Average (R_a)

The arithmetic average deviation of the absolute values of the roughness profile from the mean line or centerline. Also known as Centerline Average Roughness. *See* Centerline.

Roughness Height (R_h)

The difference in height in the roughness profile between the values at the left and right cursor positions of the profile.

SD

See Std Dev Heights.

SECS Interface

The Semiconductor Equipment Controller Standard (SECS) Interface provided on the Tencor P-20h defines a computer-to-computer communications interface between the Tencor P-20h and a host computer.

 S_m

See Mean Peak Spacing.

Sampling Length

The length of trace between the cursors.

SECS

Acronym for Semiconductor Equipment Communication Standard.

Segmented Scan

The scan is divided into segments of equal length and no data is taken between the segments. Using this method, roughness can be measured over several short lengths spaced equally along a straight line.

Select

To highlight an item by clicking it with the mouse or by using the keypad.

Selection bar

The highlighted bar or dotted rectangle appearing in a dialog box that indicates the option or command button that is selected if you press the ENTER key. The selection bar can be moved by using the keypad.

Sequence

A program of sequential scans to be performed on a single substrate.

Sequence Identifier

The Sequence ID is the name of the generating sequence program.

Six-Point Height (R_{3z})

The average height difference between the three highest peaks and the three deepest valleys within the cursors measured from a line parallel to the mean line and not crossing the profile.

Slope

The ratio of the difference in vertical positions to the difference in horizontal positions of the measurement cursors. The slope is reported as an angle in degrees.

Spatial resolution

Spatial resolution is a measure of a profiler's capability to resolve the smallest vertical or horizontal feature on a surface. Four primary factors determine spatial resolution: stylus radius, short wave filtering, vertical resolution, and horizontal resolution. In practice, stylus radius and short wave filtering are the two factors that limit spatial resolution.

Std Dev Heights (SD)

The standard deviation of the local peak heights of the roughness trace about the mean peak height within the sampling length.

StpWt

See Width of Step.

Stylus Force

The force of the stylus tip when the stylus is in contact with the substrate.

t_p

See Bearing Ratio.

TIR

See Total Indicator Runout.

Ten-Point Height (R_z)

The average height difference between the five highest peaks and the five deepest valleys within the cursors measured from a line parallel to the mean line.

Text cursor

The vertical straight line appearing in fields. The text cursor marks the location where characters appear when typed.

Title bar

Each application displays a title bar at the top of the application window. The title bar shows the application name, current recipe in parentheses, communication mode—Local or Remote—and window control buttons.

Top Level Menu

The Tencor P-20h Top Level menu displays icons of the applications available to the user.

Total Indicator Runout (TIR)

The difference in height between the highest and the lowest points within the surface bracketed by the cursors.

Type

Type identifies the type of data that can be saved, recalled, restored, or deleted in a sequence. The following six preset values are available: raw trace data, point data, sequence results, 3D data, and any data. Statistics data is supplied within sequence results.

UpBase

The bottom of the sloping side of a step-like feature, or upward step.

UpEdge

The top of the sloping side of a step-like feature, or upward step.

Upload

Exporting a recipe or data set to a remote host through the GEM/SECS Option.

Valley

The distance between the mean line and the lowest valley of the roughness or waviness trace within the sampling length.

 W_a

See Waviness Average.

 W_h

See Waviness Height.

 W_p

See Peak.

 W_q

See Root-Mean-Square Waviness.

 W_t

See Peak/Valley.

 W_v

See Valley.

Waviness

Waviness of a surface is a periodic deviation from flatness, where the wavelengths generally range from 30 to more than 100 times the average wavelength of the roughness. *See* Form Error and Roughness.

Waviness Average (W_a)

The arithmetic average deviation of the absolute values of the waviness profile from the mean line or centerline. Also known as Centerline Average Waviness. *See* Centerline.

Waviness Height (W_h)

The difference in height in the waviness profile between the values at the left and right cursor positions of the profile.

Width of Step ($StpWt$)

The distance between the first rising edge and the next falling edge of a step height plateau.

Window

Rectangular area for displaying and running an application program. The Scan application displays the Scan window.

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